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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 13:38:24 ; Search time 1844.31 Seconds
(without alignments)
11219.411 Million cell updates/sec

Title: US-09-576-424-9

Perfect score: 711

Sequence: 1 atgagggtcccgctcagct.....ccctacagaatgttcacga 711

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum Match 100%

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pi.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pi.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_hngo_hum.*

40: em_hngo_mus.*

41: em_hngo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	711	100.0	711	6	ARI08866	ARI08866 Sequence
2	582.6	81.9	935	6	ARI135362	ARI135362 Sequence
3	575.4	80.9	790	9	AB064208	AB064208 Homo sapi
4	573	80.6	870	9	HSIGLV	X14583 Human mRNA
5	571.2	80.3	903	9	BC020233	BC020233 Homo sapi
6	570.6	80.3	827	9	AB064143	AB064143 Homo sapi
7	566.6	79.7	800	9	AB064188	AB064188 Homo sapi
8	566.4	79.7	919	9	BC022098	BC022098 Homo sapi
9	566	79.7	919	9	AB064149	AB064149 Homo sapi
10	562.8	79.2	812	9	AB064148	AB064148 Homo sapi
11	562.8	79.2	816	9	AB064147	AB064147 Homo sapi
12	562.4	79.1	827	9	AB064219	AB064219 Homo sapi
13	562.2	79.1	750	9	HSIGVL027	X57817 Human rearr
14	560	78.8	747	9	HSIGVL006	X57806 Human rearr
15	558	78.5	821	9	AB064141	AB064141 Homo sapi
16	558	78.5	824	9	AB064227	AB064227 Homo sapi
17	557.6	78.4	804	9	AB064172	AB064172 Homo sapi
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19	556.4	78.3	824	9	AB064226	AB064226 Homo sapi
20	555.4	78.1	827	9	HSIGVL021	X57811 Human rearr
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23	554.4	78.0	803	9	AB064166	AB064166 Homo sapi
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26	552.8	77.7	789	9	AB064170	AB064170 Homo sapi
27	552.8	77.7	819	9	AB064151	AB064151 Homo sapi
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31	548.4	77.1	831	9	AB064224	AB064224 Homo sapi
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36	545	76.7	789	9	AB064205	AB064205 Homo sapi
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ALIGNMENTS

RESULT 1	ARI08866	ARI08866	711 bp	DNA	linear	PAT 14-FEB-2001
LOCUS	Sequence	Sequence 9	from patent US 6113898.			
DEFINITION	ARI08866					
ACCESSION	ARI08866					
VERSION	ARI08866.1	GI:12825142				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 711)					
AUTHORS	Anderson, D.R., Brams, P., Hanna, N., Shestowsky, W.S. and Heard, C.					
TITLE	Human B7.1-specific primatized antibodies and transfectomas					
JOURNAL	expressing said antibodies					
	Patent: US 6113898-A 9 05-SEP-2000;					

FEATURES Location/Qualifiers
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BASE COUNT 160 a 226 c 193 g 132 t
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Query Match 100.0%; Score 711; DB 6; Length 711;
Best Local Similarity 100.0%; Pred. No. 4.9e-174;
Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 ATGAGGGTCCCGCTCAGCTCCTGGGGCTCCTGCTGCTGCTCCAGGTGCACGATCT 60
QY 61 GAGTCTGTCTGACACAGCGCGCTCAGTGTCTGGGGCCCCAGGGCAGAGGTTCACCATC 120
Db 61 GAGTCTGTCTGACACAGCGCGCTCAGTGTCTGGGGCCCCAGGGCAGAGGTTCACCATC 120
QY 121 TGTGCACTGGGAGCACTTCCAACTATGGAGGTATGATCTACATTGGTACCAGCAGCTC 180
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RESULT 2
AR135362
LOCUS
DEFINITION
Sequence 20 from patent US 6135941.
ACCESSION
AR135362.1
KEYWORDS
GI:14476034
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 935)
AUTHORS
Hillman,J.L., Lal,P., Tang,Y.Tom., Yue,H., Au-Young,J.,
Corley,N.C., Guegler,K.J. and Baughn,M.R.
TITLE
Human immune system associated molecules

JOURNAL Patent: US 6135941-A 20 24-OCT-2000;
FEATURES Location/Qualifiers
source l. .935
BASE COUNT 216 a 299 c 248 g 172 t
ORIGIN
Query Match 81.9%; Score 582.6; DB 6; Length 935;
Best Local Similarity 89.8%; Pred. No. 1.1e-140;
Matches 637; Conservative 0; Mismatches 69; Indels 3; Gaps 1;
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QY 64 TCTGTCTTGACACAGCGCGCTCAGTGTCTGGGGCCCCAGGGCAGAGGTTCACCATCTCG 123
Db 134 TCTGTCTTGACACAGCGCGCTCAGTGTCTGGGGCCCCAGGGCAGAGGTTCACCATCTCC 193
QY 124 TGCCTGGGAGCACCTCCAACATTGG---AGGTTATGATCTATGATCTATGTTGGTACCAGCAGCTC 180
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QY 181 CCAGGAACGGCCCCAACTCCTCATCTATGACATTAAACAGCGCCCTCAGGAATTTCT 240
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RESULT 3
AB064208
LOCUS
DEFINITION
Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
region, partial cds, clone:L68.
ACCESSION
AB064208
VERSION
AB064208.1
KEYWORDS
GI:21669622
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
REFERENCE
1
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Miura, K. and Kurosawa, Y.
Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Unpublished
2 (bases 1 to 800)
Kurosawa, Y.

Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyosake 470-1192, Japan
(E-mail: kurosawa@fujita-hu.ac.jp, Tel: 81-562-93-9387)
Please visit our web site
URL: <http://www.fujita-hu.ac.jp/immunity/>.

COMMENT

FEATURES

SOURCE

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/note="pelB signal peptide"

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Best Local Similarity 93.5%; Pred. No. 1.6e-136;
Matches 603; Conservative 0; Mismatches 39; Indels 3; Gaps 1;

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RESULT 8

BC022098

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 919)

Direct Submission

TITLE

JOURNAL

Submitted (24-JAN-2002) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis Staudt

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Genome Sequence Centre,

BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,

Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,

Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo

Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven

Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline

Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott,

Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,

George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IPAL plate: 40 Row: n Column: 11

This clone was selected for full length sequencing because it

passed the following selection criteria: Genomescan gene

prediction, similarity but not identity to protein.

FEATURES

Location/Qualifiers

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/db_xref="taxon:9606"

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/note="Vector: pOTB7"

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Db 608 ACCTGAGCTGAGCGCTGAGAGTGGAGTCCACAGAAGCTACAGCTCCAGGTCAGGT 667
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RESULT 10
LOCUS AB064148
DEFINITION Homo sapiens IGL mRNA for immunoglobulin lambda light chain VLJ
AB064148
ACCESSION AB064148
VERSION AB064148.1 GI:21669502
KEYWORDS
SOURCE
ORGANISM Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,
Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,
Miura, K. and Kurosawa, Y.
TITLE Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL Unpublished
REFERENCE 2. (bases 1 to 812)
AUTHORS Kurosawa, Y.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
Comprehensive Medical Science, Fujita Health University;
Kutsukake-cho, Toyosake 470-1192, Japan
(E-mail: kurosawafujita-hu.ac.jp, Tel: 81-562-93-9387)
COMMENT Please visit our web site.
URL: http://www.fujita-hu.ac.jp/immunity/.
FEATURES
Location/Qualifiers
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REFERENCE
AUTHORS Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M.,
Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J.,
Miura, K. and Kurosawa, Y.
TITLE Construction and characterization of antibody libraries: isolation
of therapeutic human antibodies and application to functional
genomics
JOURNAL Unpublished
REFERENCE 2. (bases 1 to 816)
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AUTHORS Kurosawa, Y.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyooka 470-1192, Japan
 (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
 COMMENT Please visit our web site
 URL:http://www.fujita-hu.ac.jp/immunity/
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS
 Akahori, Y., Iba, Y., Morino, K., Shinohara, M., Hirono, Y., Kakita, M., Suzuki, K., Torii, H., Ukai, Y., Honda, T., Katsumi, H., Okada, J., Miura, K. and Kurosawa, Y.
 TITLE Construction and characterization of antibody libraries: isolation of therapeutic human antibodies and application to functional genomics
 JOURNAL Unpublished
 REFERENCE 1 (bases 1 to 827)
 AUTHORS Kurosawa, Y.
 TITLE Direct Submission
 JOURNAL Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for Comprehensive Medical Science, Fujita Health University; Kutsukake-cho, Toyooka 470-1192, Japan
 (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
 COMMENT Please visit our web site
 URL:http://www.fujita-hu.ac.jp/immunity/
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HSIGVL027 750 bp mRNA linear PRI 20-JUL-1995
Human rearranged immunoglobulin lambda light chain mRNA.
X57817
X57817.1 GI:33733
Ig lambda light chain; immunoglobulin.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Klobeck, H.G.
Direct Submission
Submitted (31-JAN-1991) H.G. Klobeck, Inst fuer Physiologische
Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
2 (bases 338 to 384)
Combratio, G. and Klobeck, H.G.
V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
Eur. J. Immunol. 21 (6), 1513-1522 (1991)
91257162
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For overlapping sequences see: X51754-55; J00252-54; M15641-42.
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REFERENCE 1. (bases 1 to 747)
AUTHORS Klobbeck,H.G.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-1991) H.G. Klobbeck, Inst fuer Physiologische
Chemie, Physikalische Biochemie und Zellbiologie der Universitaet
Muenchen, Shillerstr. 44, 8000 Muenchen 2, Germany
REFERENCE 2. (bases 335 to 381)
AUTHORS Combratio,G. and Klobbeck,H.G.
TITLE V lambda and J lambda-C lambda gene segments of the human
immunoglobulin lambda light chain locus are separated by 14 kb and
rearrange by a deletion mechanism
JOURNAL Eur J Immunol. 21 (6), 1513-1522 (1991).
MEDLINE 91257162
PUBMED 1904362
COMMENT for overlapping sequences see: X51754-55; J00252-54; M15641-42.
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VERSION AB064141.1 GI:21669488
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SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1.
AUTHORS Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
11875.950 Million cell updates/sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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REFERENCE 1 (bases 1 to 956)
NIH-MGC <http://mgi.nci.nih.gov/>
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: AGencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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High quality sequence start: 10
High quality sequence stop: 655.
Location/Qualifiers

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/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="IMAGE:6278335"
/lab_host="NIH_MGC_113"
/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."

BASE COUNT 218 a 256 g 172 t 7 others
ORIGIN

Query Match 80.1%; Score 569.2; DB 14; Length 956;

Best Local Similarity 88.6%; Pred. No. 4.2e-142;

Matches 629; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

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QY 3 GAGGGTCCCGCTCAGCTCTGGGGCTCTCGTCTGCTGCTCCAGGTGCAGATGTA 62
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Db 22 GATGGCTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 81
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QY 63 GTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCGAGGGCAGAGGTACCATCTC 122
  |||
Db 82 GTCTGTCTGACAGCGCCCTCAGTGTCTGGGGCCCGAGGGCAGAGGTACCATCTC 141
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QY 123 GTGCTGAGGAGCAGCTTCAACATTTGG---AGTTATGATCTATTTGGTACAGAGCT 179
  |||
Db 142 CTGCACTGGGAGCAGCTTCAACATTTGGTGTGATGTTGTTGTTGTTGTTGTTGTT 201
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QY 180 CCAGGAGCGGCCCCCAACTCTCTATCTATGATTAACAGCGACCTTCAGGAATTC 239
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Db 202 TCAGGAAGACGCCCCCAACTCTCTATCTATGATTAACAGCGAATTCAGGGTCC 261
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QY 240 TGACCGATTCTCTGGGTCCAAAGTCTGGTACCGGGCTCTCTGGCCATCACTGGGTCCA 299
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QY 480 AAGTGACTTCTACCCGGAGCCGTGACAGTGGCTTGAAGGCGATAGCAGCCCCGTCAA 539
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QY 600 CTACCTGAGCTTACGCTGAGCAGTGAAGTCTCCACAGAGCTTACAGTGGCCAGGTTCAC 659
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Db 622 CTACCTGAGCTTACGCTGAGCAGTGAAGTCTCCACAGAGCTTACAGTGGCCAGGTTCAC 681
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QY 660 GCATGAAGGAGCAGCCGTGGAGAGCAGTGGCCCCCTTACAGATGTTTCAT 709
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Db 682 GCATGAAGGAGCAGCCGTGGAGAGCAGTGGCCCCCTTACAGATGTTTCAT 731
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RESULT 2

BQ708635

LOCUS

BQ708635 913 bp mRNA linear EST 16-JUL-2002

DEFINITION

AGENCOURT_8351417 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6282312

5', mRNA sequence.

ACCESSION BQ708635

VERSION BQ708635.1 GI:21847534

KEYWORDS EST.

SOURCE human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 913)

NIH-MGC http://mgc.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Mark Watson

cDNA Library Preparation: Rubin Laboratory

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLM2476 row: i column: 01

High quality sequence stop: 663.

FEATURES

source

1. .913

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6282312"

/lab_host="NIH MGC_113"

/note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:

EcoRI; cDNA made by oligo-dT priming. Directionally cloned

into EcoRI/XhoI sites using the following 5' adaptor:

GGCACAG(G). Library constructed by Ling Hong in the

Laboratory of Gerald M. Rubin (University of California,

Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and

Superscript II RT (Life Technologies). Note: this is a

NIH MGC Library."

BASE COUNT 214 a 301 c 230 g 167 t 1 others

ORIGIN

Query Match 79.1%; Score 562.6; DB 14; Length 913;

Best Local Similarity 88.9%; Pred. No. 2.5e-140;

Matches 631; Conservative 0; Mismatches 75; Indels 4; Gaps 2;

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Db 36 ATGGGCTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 95
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Db 156 TGCACCTGGGAGCAGCTTCAACATCGGGCAGGTTATATGATGATGATGATGATGATGAT 215
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QY 181 CCAGGAACGGCCCCCAACTCTCATATGATTAACAAAGGACCCCTCAGGAATTTCT 240
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Db 216 CCAGGAACAGCCCCCAACTCTCATATGATTAACAAAGGACCCCTCAGGGGTCCCT 275
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QY 241 GACCATTTCTGGGTCCCAAGTCTGGTACCGGGCTCTCTGGCCATCACTGGGTCCAG 300
  |||
Db 276 GACCATTTCTGGGTCCCAAGTCTGGTACCGGGCTCTCTGGCCATCACTGGGTCCAG 335
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QY 301 ACTGAGGATGAGCTGATTTACTGCCAGTCTCTATGACAGCAGCTTGAATGCTCAGGTA 360
  |||
Db 336 GCTGAGGATGAGCTGATTTACTGCCAGTCTCTATGACAGCAGCTTGAATGCTGAGTG 395
  |||
QY 361 TTCGAGGAGGAGCAGCGGTGACCGTCTTAGTTCAGGCCCAAGGCTGCCCTCGGTCACT 420
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Db 396 TTCGCGGAGGAGCAGCGGTGACCGTCTTAGTTCAGGCCCAAGGCTGCCCTCGGTCACT 455
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Query Match	78.1%;	Score 555.6;	DB 12;	Length 755;
Best Local Similarity	89.5%;	Pred. No. 1.8e-138;		
Matches 621; Conservative 0;	Mismatches 69;	Indels 4;	Gaps 2;	

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Db	21	ATGGCCCTGGGTCTCTCTTCCTCCTCACTCTCTCTCGCTCACTGCACAGGGTCTCTGGGCCCGAG	80
Qy	64	TCTGTCTCTGACACAGCGCCGCTCAGTGTCTGGGGCCCCAGGGCAGAAGSTCACCATCTCG	123
Db	81	TCTGTCTGACGACGCGCCCTCAGTGTCTGGGGCCCCA-GGCAGAGGGTCACCATCTCC	139
Qy	124	TGCACCTGGGAGCACCTCCAATTGG--AGGTTATGATCTACAATTGGTACACAGAGCTC	180
Db	140	TGCACCTGGGAGCAGCTCAAATCGGGCAGGTTATGATGTATCACTTGGTATCACAGCAGCTT	199
Qy	181	CCAGGAACGGCCCCAAACTCCTCATCTATGACATTAAACAGCGACCCCTCAGGAATTCT	240
Db	200	CCAGGAACAGCCCCAAACTCCTCATCTATGTTAACAGCAATCGGCCCTCAGGGGTCCCT	259
Qy	241	GACCGATTCTCTGGCTCCAAAGTCTGGTACCGCGGCCTCCCTGGGCATCACTTGGGCTCCAG	300
Db	260	GACCGATTCTCTGGCTCCAAAGTCTGGCACCTCAGCCTCCCTGGCCATCACTTGGGCTCCAG	319
Qy	301	ACTGAGGATGAGGCTGATTAATTACTGCCAGTCTTATGACAGCAGCGCTGAATGCTCAGGTA	360
Db	320	GCTGAGGATGAGGCTGATTAATTACTGCCAGTCTTATGACAGCAGCGCTGAGTGGTGGGGTG	379
Qy	361	TTCCGAGGAGGGACCGGCTGACCGTCTTAGGTGAGCCCAAGGCTGCCCTTCGGTCACT	420
Db	380	TTCCGCGGAGGGACCAAGCTGACCGTCTTAGTTCAGCCCAAGGCTGCCCTTCGGTCACT	439
Qy	421	CTGTTCCTCGGCCCTCCTCTGAGGAGCTTCAAGCCAAAGGCCACAACCTGGTGTCTCATATA	480
Db	440	CTGTTCCTCGGCCCTCCTCTGAGGAGCTTCAAGCCAAAGGCCACAACCTGGTGTCTCATATA	499
Qy	481	AGTGACTTCTTACCCGGAGCCGTGACAGTGGCTTGGAAAGGCAGATAGCAGCCCCGTCAAG	540
Db	500	AGTGACTTCTTACCCGGAGCCGTGACAGTGGCTTGGAAAGGCAGATAGCAGCCCCGTCAAG	559
Qy	541	GCGGAGTGGAGACCACACACCTCCAAACAAGCAACACNAAGTACGCGGCCAGCAGC	600
Db	560	GCGGAGTGGAGACCACACACCTCCAAACAAGCAACACNAAGTACGCGGCCAGCAGC	619
Qy	601	TACCTGAGCCTGAGCCCTGAGCAGTGGAAAGTCCCACAGAAGCTACAGCTGCCAGGTCAAG	660
Db	620	TATCTGAGCCTGAGCCCTGAGCAGTGGNAGTCCCACAGNAGCTACAGCTGCCAGGTCAAG	679
Qy	661	CATGAAGGGAGCACCGTGGGAGAAGACAGTGGCCC	694
Db	680	CATGAAGGGAGCACCGTGGGAGAAGACAGTGGCCC	713

RESULT 7	BM920020	1007 bp	linear	mRNA	EST 12-MAR-2002
LOCUS	BM920020	ACENGCOURT_6708356	NIH_MGC_120	Homo sapiens	cdna clone IMAGE:5749866
DEFINITION	5', mRNA sequence.				
ACCESSION	BM920020				
VERSION	BM920020.1				
KEYWORDS	GI:19370399				
SOURCE	EST.				
ORGANISM	human.				
	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 1007)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/ .				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc.				

cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 plate: LLNL12779 row: 0 column: 14
 High quality sequence stop: 712.

FEATURES	source
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/clone="IMAGE:5749861"	
/clone_lib="NIH MGC_120"	
/lab_host="DH10B"	
/note="Organ: pooled pancreas and spleen; Vector: pcMV-SPOK6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dr primed and directionally clone (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH MGC Library."	
253 a	336 c 232 g 173't 13 others
BASE COUNT	

Query Match 77.7%; Score 552.2; DB 14; Length 1007;
Best Local Similarity 86.2%; Pred. No. 1.6e-137;
Matches 611; Conservative 0; Mismatches 98; Indels 0; Gaps 0

Qy	1	ATGAGGGTCCCGCTCAGCTCTCGGGGCTCTGCTGCTCTGGCTCCGAGTGACGANGT	60
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Qy	61	GAGTCTGTCTGCACAGCGCGCCTCAGTGTCTGGGGCCCGCAGGCGAAGGTCACCATC	120
Db	89	CAGTCTGTGTTGACGAGCGCGCCTCAGTGTCTGGGCCCGCAGACAGGGTCAACATC	148
Qy	121	TGCTGCATCTGGGAGCACTTCCAACTATTTGGAGGTTATGATTTACATTTGGTACCAAGAGCTC	180
Db	149	TCTCTGCTCTGGAAGGAGCTTCCAACTTTGGAATAGTTATGTGTCTCTGGTATCAGCAGTTC	208
Qy	181	CCAGGAAACGGCCCCCAACTCTCTCATCTATGACATTTAAACAGCGACCTCAGGAATTTCT	240
Db	209	CCAGGAGCAGCCCCCACTCTCTCATTTATGACATGATAGCGACCTCAGGGATTTCT	268
Qy	241	GACCGATTCTTGGCTCOAGTCTGGTACCGGGGCTCCCTGGCCATCACTGGGCTCCAG	300
Db	269	GACCGATTCTTGGCTCCAGTCTGGCAGCTCAGCACCTCTGGCCATCAGCGACTCCAG	328
Qy	301	ACTGAGGATGAGCTGATTATTACTTGCAGTGCTTATGACAGCAGCCTGAATGCTCAGGTA	360
Db	329	ACTGAGGACGAGCCGAACTACTTTCGGAACTGGGATACAGCTGACTGCTGGGGTT	388
Qy	361	TTCGGAGGAGGACCGGGCTGACCTTCTTAGTTCAGGCCAAGGCTGCCCTCGTCACT	420
Db	389	TTCCGGCGTGGGACCAAACTGACCGTCTTAAGTCAGCCAGGCTGCCCTCGTCACT	448
Qy	421	CTGTTCCTCCGCTCTCTCTGAGAGCTTCAAGCCACAGGCGCACACTGGTGTCTCATTA	480
Db	449	CTGTTCCTCCGCTCTCTCTGAGAGCTTCAAGCCACAGGCGCACACTGGTGTCTCATTA	508
Qy	481	AGTGACTTCTACCCGGAGCCGTGACAGTGGCTTGGAGGCAGATAGCAGCCCCGTCAAG	540
Db	509	AGTGACTTCTACCCGGAGCCGTGACAGTGGCTTGGAGGCAGATAGCAGCCCCGTCAAG	568
Qy	541	GGGGAGTGGAGACCAACACCTTCCAAACAAAGCAACAGTACGGGGCAGCAGC	600
Db	569	GGGGAGTGGAGACCAACACCTTCCAAACAAAGCAACAGTACGGGGCAGCAGC	628
Qy	601	TACCTGAGCTCAGCGCTGAGCAGTGGGAAGTCCCAAGAACTACAGTCCGAGGTCAAG	660

Db	629	TATCTGAGCCTGAGCGCTGAGCAGTGGAGAGTCCCA	CAGAGACTACAGCTGCCAGGTCA	CAG 688
Qy	661	CATGAAGGGAGCACCCTGGAGAGACAGTGGCCCCCTACAGAA	TGTTTCAT 709	
Db	689	CATGAAGGGAGCACCCTGGAGAGACAGTGGCCCCCTACAGAA	TGTTTCAT 737	

RESULT 8	BM906351	1060 bp	mRNA	linear	EST 12-MAR-2002
LOCUS	AGENCOURT 6620012 NIH_MGC_125	Homo sapiens	cdna clone	IMAGE:5590299	
DEFINITION	5', mRNA sequence.				
ACCESSION	BM906351				
VERSION	BM906351.1	GI:19356730			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
TITLE	1 (bases 1 to 1060)				
JOURNAL	NTH-MGC http://mgc.nci.nih.gov/ .				
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)				
	Unpublished (1999)				
	Contact: Robert Strausberg, Ph.D.				
	Email: cgapbs-remail.nih.gov				
	Tissue Procurement: Invitrogen				
	cdna Library Preparation: Life Technologies, Inc.				
	cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)				
	dna Sequencing by: Agencourt Bioscience Corporation				
	Clone distribution: MGC clone distribution information can be				
	found through the I.M.A.G.E. Consortium/LLNL at:				
	http://image.llnl.gov				
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FEATURES
source

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/clone="IMAGE:5590299"
/clone_lib="NIH MGC 125"
/lab_host="DH10B"
/notes="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
Site 1: EcoRV (destroyed); Site 2: NotI; RNA source: pool
of three ovaries, from females ranging in age from 38 to
49 yo. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 2.1 kb, insert size range 1-3.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 036."

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ORIGIN					

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Best Local Similarity	86.2%;	Pred. No. 1.6e-137;		
Matches 611;	Conservative	0;	Mismatches 98;	Indels 0;
				Gaps 0;

Qy	1	ATGAGGGTCCCCGTGAGCTCTCTGGGGCTCCTGCTGCTCTGGCTCCCGAGTGACAGATGT	60
Db	49	ATCATGACCTGCTCCCTCTCTCTCCCTCCTCAGCCCTTCTCATTTCACTGACACAGGGTCTCTGGGCC	108
Qy	61	GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGCGGGCCCCAGGGGACGAGGTCACCATC	120
Db	109	CAGTCTGTGTGACAGCGCCCTCAGTGTCTGCGGCCCCGAGACAGGAGGGTCAACGGTC	168
Qy	121	TCGTGCACCTGGGAGCACCTCCAACTATTGGAGGTTATGATCTACATTTGGTACCAGCAGCTC	180
Db	169	TCCTGCTCTGGAGCAGTGCACACATTTGGAGTAATTTAGTTTCTGTGTACCAACCTC	228
Qy	181	CCAGGAACGGCCCCCAACTCTCTCATCTATGACATTTAAAGCGACCCCTCAGGAATTTCT	240
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 QY 301 ACTGAGATGAGCTGATTACTGCGAGTCTATGACAGCAGCTGAAATGCTCAGGTA 360
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 QY 361 TTCGGAGGAGGACCGGCTGACCGTCTTAGGTGAGCCCAAGCTGCGCTCGGTCACT 420
 Db 409 TTCGGGCGGAGACCAAACTGACCGTCTTAGGTGAGCCCAAGCTGCGCTCGGTCACT 468
 QY 421 CTGTTCCGCGCTCTCTGAGGAGCTTCAAGCCCAAGCCACACTGGTGTGTCTCAT 480
 Db 469 CTGTTCCGCGCTCTCTGAGGAGCTTCAAGCCCAAGCCACACTGGTGTGTCTCAT 528
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 QY 661 CATGAAGGAGACCGGTGAGAGAGACAGTGGCGCCCTACAGAATGTTTCAAT 709
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 VERSION 1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cga@rs-rcmail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
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 /tissue_type="primary B-cells from tonsils (cell line)"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp
 for average insert size 1.8kb. Library constructed by Ling

FEATURES

source

RESULT 10

BQ890529

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 857)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NIH-MGC http://mgi.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@rs-rcmail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.llnl.gov

Plate: L1CM1692 row: p column: 03

High quality sequence stop: 879.

Location/Qualifiers

1..910

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/db xref="taxon:9606"

/clone="IMAGE:4850930"

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/tissue_type="primary B-cells from tonsils (cell line)"

/lab_host="DH10B (phage-resistant)"

/note="Organ: B-cells; Vector: pOTB7; Site 1: XhoI;

Site 2: EcoRI; cDNA made by oligo-dT priming.

Directionally cloned into EcoRI/XhoI sites using the

following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by Ling

Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library.
 BASE COUNT 218 a 295 c 229 g 168 t
 ORIGIN

Query Match 77.6%; Score 551.6; DB 12; Length 910;

Best Local Similarity 88.9%; Pred. No. 2.2e-137;

Matches 631; Conservative 0; Mismatches 74; Indels 5; Gaps 3;

QY 4 AGGGTCCCCGCTCAGCTCCTGGGGCTCCTGGCTCTGGCTCCAGGTGACGATGTGAG 63
 Db 36 ATGGCTGGTCT 95
 QY 64 TCTGTCTCTGACACAGCGGCTCAGTGTCTTGGGGGCCCCAGGCGAGAGGTCAACATCTCG 123
 Db 96 TCTGTCTCTGACGAGCGGCTCAGTGTCTTGGGGGCCCCAGGCGAGAGGTCAACATCTCC 155
 QY 124 TGCACTGGGAGACCTTCCAAACATTTG---AGTTATGATCTACATTGGTACCGAGCTC 180
 Db 156 TGCACTGGGAGAGCTTCCAAACATCGGGGCGAGGTATGTTGTTTCTTATGTTATCAGCAGCTT 215
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 Db 516 AGTGACTTCTACCCGGGAGCGGTGACAGTGGCTGGAAGGACAGATAGCAGCCCGTCAAG 575
 QY 541 GCGGGAGTGAGACCAACACCTTCCAAACAAGCAACAAGTACGCGGCGCAGCAGC 600
 Db 576 GCGGGAGTGAGACCAACACCTTCCAAACAAGCAACAAGTACGCGGCGCAGCAGC 634
 QY 601 TACTGAGCTGAGCAGC-CCTGAGCAGTGGAGTCCCAAGAGCTTACAGCTGCGCAGGTGAC 659
 Db 635 TACTGAGCTGAGCAGCCTGAGCAGTGGAGTCCCAAGAGCTTACAGCTGCGCAGGTGAC 694
 QY 660 GCATGAAGGAGGACCGGTGAGAGAGCAGTGGCGCCCTTACAGAATGTTTCAAT 709
 Db 695 GCATGAAGGAGGACCGGTGAGAGAGCAGTGGCGCCCTTACAGAATGTTTCAAT 744

BQ890529 857 bp mRNA linear EST 16-AUG-2002
 AGENCOURT 858752 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302538
 5', mRNA sequence.

BQ890529

BQ890529.1 GI:22282543

EST.

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 857)


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Db 159 TCCTGCTCTGGAAGCAGGTCACATTTGGGAATAATTATGTCTGCTGGTACCAGCAGCTC 218
Qy 181 CAGGAAACGGCCCGCCAACTCTCACTATGACATTAACAAAGCGACCTCAGGAATTTCT 240
Db 219 CAGAGTACAGCCCGCAACTCTCTCATATGAAATAGTAGGCGACCTCAGGGAATCTT 278
Qy 241 GACCGATTCTCTGCTCCAGTCTGGTACCGCGCTCCCTGCGCATCACTGGGCTCCAG 300
Db 279 GACCGATTCTCTGCTCCAGTCTGGTACCGCGCTCCCTGCGCATCACTGGGCTCCAG 338
Qy 301 ACTGAGGATGAGGCTGATTATTAAGTCTGACAGCAGCCTGGAATGCTCAGGTA 360
Db 339 ACTGGGACGAGCGCGATTATTAAGTCTGGAACATGGATGACAGCCTGCGTGTGGTG 398
Qy 361 TTGCGAGGAGGACCGCGCTGACCGTCTTAGTTCAGCCAAAGCTGCGCCCTCGGTCACT 420
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Qy 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGCCCACTGTTGTCTCATTA 480
Db 459 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGCCCACTGTTGTCTCATTA 518
Qy 481 AGTGACTTCTACCCGGAGCGGTGACAGTGGCTTGAAGGCAGATAGCAGCCCGCTCAAG 540
Db 519 AGTGACTTCTACCCGGAGCGGTGACAGTGGCTTGAAGGCAGATAGCAGCCCGCTCAAG 578
Qy 541 GCGGAGTGAGACCAACACCCCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 600
Db 579 GCGGAGTGAGACCAACACCCCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 638
Qy 601 TACCTGAGCTGAGCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTCCAGGTCAGC 660
Db 639 TACCTGAGCTGAGCGCTGAGCAGTGGAGTCCACAGAGCTACAGCTCCAGGTCAGC 698
Qy 661 CATGAAGGAGCAGCCGTTGGAAGAGACAGTGGCCCTTACAGAAATGTTCCAT 709
Db 699 CATGAAGGAGCAGCCGTTGGAAGAGACAGTGGCCCTTACAGAAATGTTCCAT 747
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RESULT 12

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BI835917 817 bp mRNA linear EST 04-OCT-2001
LOCUS 603085650F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5224645 5',
DEFINITION mRNA sequence.
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ACCESSION BI835917
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VERSION BI835917.1 GI:15947467
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KEYWORDS EST.
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SOURCE human.
```

ORGANISM

```
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 817)
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```
NIH-MGC http://mgi.nci.nih.gov/
```

```
National Institutes of Health, Mammalian Gene Collection (MGC)
```

```
Unpublished (1999)
```

```
Contact: Robert Strausberg, Ph.D.
```

```
Email: cgapbs-r@mail.nih.gov
```

```
Tissue Procurement: Life Technologies, Inc.
```

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cDNA Library Preparation: Life Technologies, Inc.
```

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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
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DNA Sequencing by: Incyte Genomics, Inc.
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Clone distribution: MGC clone distribution information can be
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found through the I.M.A.G.E. Consortium/LNLN at:
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http://image.llnl.gov
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Plate: L1AM11565 row: C column: 14
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High quality sequence stop: 817.
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Location/Qualifiers
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1. 817
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/clone="IMAGE:5224645"
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/clone_lib="NIH_MGC_120"
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/lab_host="DH10B"
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FEATURES

```
source
```

```
RESULT 13
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BG685967
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```
LOCUS
```

```
DEFINITION
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602638530F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766335 5',
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mRNA sequence.
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ACCESSION BG685967
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VERSION BG685967.1 GI:13917364
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KEYWORDS EST.
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/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT 188 a 265 c 210 g 154 t

ORIGIN

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Query Match 76.8%; Score 546; DB 13; Length 817;
Best Local Similarity 86.5%; Pred. No. 6.9e-136;
Matches 614; Conservative 0; Mismatches 95; Indels 1; Gaps 1;

Qy 1 ATGAGGGTCCCCCTCAGCTCTGGGGCTCTCTGCTCTGCTGCTCCAGGTGACAGATGT 60
Db 30 ATCATGACCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 89
Qy 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCCCAGGGGAGAAAGGTCAACATC 120
Db 90 CAGTCTGTGTGAGCAGCGCGCCCTCAATGTCTGTGGGGCCCCCTGACACAGAAAGGTCTCCATC 149
Qy 121 TCGTGACCTGGGAGCAGCTCCAAATTTGAGGTTATGATCTACATTTGGTACAGCAGCTC 180
Db 150 TCTGTCTCTGGAAGCAGCTCCAAATTTGAGGTTATGATCTACATTTGGTACAGCAGCTC 209
Qy 181 CAGGAAACGGCCCCCAAACTCTCTATATGACATTAACAAAGCGACCTCAGGAATTTCT 240
Db 210 CAGGAAACGGCCCCCAAACTCTCTATATGACATTAACAAAGCGACCTCAGGATTTCT 269
Qy 241 GACCGATTCTCTGGTCCAAAGTCTGTGTACCGGGCTCTCTGCTGCTGCTGCTGCTGCT 300
Db 270 GACCGATTCTCTGGTCCAAAGTCTGTGTACCGGGCTCTCTGCTGCTGCTGCTGCTGCT 329
Qy 301 ACTGAGGATGAGCTGATTTATTTACTGCGAGTCTCTATGACAGCAGCTGATGCTCAGGTA 360
Db 330 ACTGGGGACGAGCGCGGATTTATTTATTCGGAACATGGGATAGCAGCCTGAGTGTGTGCTA 389
Qy 361 TTCGAGGAGGAGGACCGCGCTGACCGTCTAGGTGACGCAAGGCTGCCCCCTCGGTCACT 420
Db 390 TTCGCGGAGGAGGACCAAGCTGACCGTCTAGGTGACGCAAGGCTGCCCCCTCGGTCACT 449
Qy 421 CTGTTCCCGCCCTCTCTCTGAGGAGCTTCAAGCCAAACAAAGGCCACACTGGTGTGTCTCATTA 480
Db 450 CTGTTCCCGCCCTCTCTCTGAGGAGCTTCAAGCCAAACAAAGGCCACACTGGTGTGTCTCATTA 509
Qy 481 AGTGACTTCTACCCGGAGCGGTGACAGTGGCTTGAAGCGAGATAGCAGCCCGCTCAAG 540
Db 510 AGTGACTTCTACCCGGAGCGGTGACAGTGGCTTGAAGCGAGATAGCAGCCCGCTCAAG 569
Qy 541 GCGGAGTGAGGAGCAGCAGCCCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 600
Db 570 GCGGAGTGAGGAGCAGCAGCCCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGC 639
Qy 601 TACCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAGCTTACAGAGCTGCTGCTGCTGCTGCT 659
Db 630 TATCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAGCTTACAGGCTGCTGCTGCTGCTGCT 689
Qy 660 GCATGAAGGAGGAGCAGCTGAGGAGAGCAGTGGGCCCTTACAGAAATGTTTAT 709
Db 690 GCATGAAGGAGGAGCAGCTGAGGAGAGCAGTGGGCCCTTACAGAAATGTTTAT 739
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BG685967

896 bp mRNA linear EST 01-MAY-2001

602638530F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4766335 5',

mRNA sequence.

BG685967

BG685967.1 GI:13917364

EST.


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QY 122 CTTGCTGGAGCAGCTCCAACTTGGAGTTATGATCTACATTTGGTACCAGCAGCTCC 181
Db 77 CTTGTTCTGAAGCAGCTCCAACTCGAAGTAATATGATATGATGTTGTTACAGCAGCTCC 136
QY 182 CAGGAACGGCCGCCCAAACTCTCATCTATGACATTAACAGCGACCTCAGGAATTTCTG 241
Db 137 CAGGAACGGCCGCCCAAACTCTCATCTATGAGTAATATGAGCGGCTCAGGGTCCCTG 196
QY 242 ACCGATTTCTGCTCCAACTTGGTACCGCGGCTCCCTGGCCATCACTGGGCTCCAGA 301
Db 197 ACCGATTTCTGCTCCAACTTGGTACCGCGGCTCCCTGGCCATCACTGGGCTCCGGT 256
QY 302 CTGAGATGAGGCTGATTAATTAATCTGAGCTCCCTATGACAGCAGCTGATCTCAGGTAT 361
Db 257 CCGAGGATGAGGCTGATTAATTAATCTGAGCTCCCTATGAGCTGAGCTGAGTGTGTTAT 316
QY 362 TCGGAGGAGGAGCCCGCTGACCGTCTAGGTGAGCCCAAGGCTGCGCCCTCGGTCACTC 421
Db 317 TCGGAGGAGGAGCCCGCTGACCGTCTAGGTGAGCCCAAGGCTGCGCCCTCGGTCACTC 376
QY 422 TGTTCGCGCTCTCTCTGAGGAGCTTCAAGCCCAAGGCTGAGTGTGTTCTATAA 481
Db 377 TGTTCGCGCTCTCTCTGAGGAGCTTCAAGCCCAAGGCTGAGTGTGTTCTATAA 436
QY 482 GTGACTTCTACCGGAGCGGTGACAGTGGCTTGGAGGAGATAGAGCCCGCTCAAGG 541
Db 437 GTGACTTCTACCGGAGCGGTGACAGTGGCTTGGAGGAGATAGAGCCCGCTCAAGG 496
QY 542 CGGAGTGGAGACCAACACCTCCAAACAAAGCAACACAGTACAGTGGCGGCGAGCT 601
Db 497 CGGAGTGGAGACCAACACCTCCAAACAAAGCAACACAGTACAGTGGCGGCGAGCT 556
QY 602 ACCTGAGCTTACCGCTGAGCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 661
Db 557 ATCTGAGCTTACCGCTGAGCAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 616
QY 662 ATGAAGGAGACCGTGGAGAGACAGTGGCGGCTTACAGATTTTCAT 709
Db 617 ATGAAGGAGACCGTGGAGAGACAGTGGCGGCTTACAGATTTTCAT 663
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RESULT 15
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DEFINITION mRNA sequence.
ACCESSION BG756887
VERSION BG756887.1 GI:14067540
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 849)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabps-i@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCW1692 row: o column: 20
High quality sequence stop: 841.
Location/Qualifiers
1..849
/organism="Homo sapiens"
/db_xref="taxon:9606"
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FEATURES
source

Search completed: June 3, 2003, 19:28:20
Job time : 974.606 secs

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BASE COUNT 202 a 280 c 213 g 154 t
ORIGIN
Query Match 76.6%; Score 544.6; DB 12; Length 849;
Best Local Similarity 87.2%; Pred. No. 1.6e-135;
Matches 620; Conservative 0; Mismatches 89; Indels 2; Gaps 2;
QY 1 ATGAGGTTCCCGCTCAGCTCTCTGGGGCTCTCTGCTCTCTGGCTCCAGGTGACCATGT 60
Db 29 ATCATGACCTGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 88
QY 61 GAGTCTGTCTGACACAGCGGCTCTCAGTGTCTGGGGCCCGGAGGAGGAGGTGACCATC 120
Db 89 CAGTCTGTCTGACGAGCGGCTCTCAGTGTCTGGGGCCCGGAGGAGGAGGTGACCATC 148
QY 121 TCGTGACCTGGGAGCAGCTCCAACTTGGAGGTTATGATCTACATTTGGTACAGCAGCTC 180
Db 149 TCTGTCTCTGGAAGCAGCTCCAACTTGGAGTAAATATGATCTCTGTTACAGCAATC 208
QY 181 CCAGGAACGGCCGCCCAAACTCTCTATGATGATTAACAAAGCGACCTCAGGAATTTCT 240
Db 209 CCAGGAACGAGCGCCCAAACTCTCTATGATGATTAACAAAGCGACCTCAGGAATTTCT 268
QY 241 GACCGATTTCTGGCT-CCAAGTCTGTACCGGGCTCTCTGGGCTCTCTCTGGGCTCCA 299
Db 269 GACCGATTTCTGGCTCCCAAGTCTGCGACGTCAGCCACCTCTGGGCTATCACCGGACTCA 328
QY 300 GACTGAGGATGAGGCTGATTATTACTGCGCAGTCTCTATGACAGCAGCTGATCTCAGGT 359
Db 329 GACTGGGAGCAGGCGGATTTACTGCGGAACATGGGATAGCAGCTGAGTCTGGGT 388
QY 360 ATTGAGGAGGAGCCCGCTGACCGTCTCTAGGTACAGCCCAAGGCTGCGGCTCTCTCTCAC 419
Db 389 GTTGGCGGAGGAGCCCAAGCTGACCGTCTCTAGTCAAGCCCAAGGCTGCGGCTCTCTCAC 448
QY 420 TCTGTTCCCGCTCTCTCTGAGAGCTTCAAGCAACAGGCGCACACTGTTGTCTCAT 479
Db 449 TCTGTTCCCGCTCTCTCTGAGGAGCTTCAAGCAACAGGCGCACACTGTTGTCTCAT 508
QY 480 AAGTGACTTTCTACCGGGAGCGTGCAGTGGCTGGAGGAGGAGATAGCAGGCGGCTCAA 539
Db 509 AAGTGACTTTCTACCGGGAGCGTGCAGTGGCTGGAGGAGGAGATAGCAGGCGGCTCAA 568
QY 540 GCGGGAGTGGAGAGCCACCACTCTCCAAACAAAGCAACAAAGTACGCGGCCAGCAG 599
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QY 600 C-TACTGTAGCTGAGCGCTGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 658
Db 629 CTTTACCTGAGCTGAGCGCTGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 688
QY 659 CGCATGAAGGAGGAGCGGCTGGAGAGACAGTGGCGGCTTACAGATTTTCAT 709
Db 689 CGCATGAAGGAGGAGCGGCTGGAGAGACAGTGGCGGCTTACAGATTTTCAT 739
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Search completed: June 3, 2003, 19:28:20
Job time : 974.606 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 13:14:13 ; Search time 158.886 Seconds
(without alignments)
10077.457 Million cell updates/sec

Title: US-09-576-424-9

Perfect score: 711

Sequence: 1 atgagggtcccgctcagct.....ccctacagaatgttcata 711

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: /SID22/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	711	19	AAV35488
2	711	100.0	711	24	AA517246
3	709.4	99.8	711	18	AA762512
4	582.6	81.9	935	22	AAC66525
5	571.4	80.4	884	11	AAQ03609
6	565.2	79.5	762	22	AAC84209
7	558.8	78.6	5679	22	AAC84207
8	552.6	77.7	768	20	AA06953
9	552.6	77.7	768	20	AA06954

10	547	76.9	654	14	AAQ49835
11	546.2	76.8	810	23	AA587270
12	540.2	76.0	705	18	AA762509
13	540.2	76.0	705	19	AAV35484
14	540.2	76.0	705	24	AA517242
15	533.2	75.0	651	19	AAV11293
16	533.2	75.0	708	22	AAH47902
17	532.2	74.9	915	24	ABN97248
18	532.2	74.9	915	24	ABK64815
19	532.2	74.9	915	24	ABL65478
20	530.2	74.6	895	22	AA666530
21	523.6	73.6	708	22	AAH47904
22	522.8	73.5	1845	24	ABL49526
23	518.8	73.0	708	22	AAH47898
24	510.6	71.8	891	22	AAC66528
25	509.2	71.6	763	23	AA583480
26	502.6	70.7	902	14	AAQ35100
27	499.4	70.2	889	23	AA577073
28	498.6	70.1	906	22	AAK51914
29	496.4	69.8	951	23	AA590539
30	494.4	69.5	783	23	AA583483
31	494.4	69.5	876	23	AA583478
32	493.8	69.5	888	21	AAA95786
33	487.4	68.6	1636	23	ABV22585
34	487.4	68.6	1636	23	ABV28405
35	486.6	68.4	756	23	AA583477
36	484.2	68.1	885	19	AAV34321
37	482.6	67.9	879	19	AAV34304
38	480.6	67.6	1636	23	ABV22585
39	480.6	67.6	1636	23	ABV28405
40	477	67.1	926	20	AAZ24427
41	475.2	66.8	807	23	AA583484
42	470.4	66.2	872	9	AAH81655
43	468.4	65.9	702	18	AA762867
44	466	65.5	1027	24	ABQ54438
45	465.6	65.5	849	22	AAH98186

ALIGNMENTS

RESULT 1

AAV35488

ID AAV35488 standard; DNA; 711 BP.

XX AC

XX AAV35488;

XX AC

XX 29-SEP-1998 (first entry)

XX DE

XX Macaque primatized 16C10 light chain DNA.

XX KW

XX Monoclonal antibody; Mab; macaque; light chain; antigen; CD80;

XX CD86; inhibitor; immunosuppressant; treatment; autoimmune disease; IL-2;

XX T cell/B cell interaction; tumour; inflammation; imaging agent; vaccine;

XX immunogen; anti-idiotype reagent; interleukin-2; Igc; immunoglobulin G;

XX T cell proliferation; ss.

XX OS

XX Macaca fascicularis.

XX FH

XX Key

XX Location/Qualifiers

XX CDS

XX 1..711

XX /*tag= a

XX /product= 16C10 light chain

XX PN

XX WO9819706-A1.

XX PD

XX 14-MAY-1998.

XX XX

XX Human immune syste

XX PF

XX Sequence encoding

XX XX

XX Plasmid Glambda-1B

XX PR

XX Plasmid Glambda-1A

XX Monoclonal antibod

XX PA

XX (IDEC-) IDEC PHARM CORP.

XX Anderson DR, Brams P, Hanna N;
 XX WPI; 1998-286601/25.
 DR P-PSDB; AAW63764.
 XX
 XX New monoclonal antibodies specific for B7.1 or B7.2 antigens and
 PT inhibiting binding to CD28 - useful as specific immunosuppressants
 PT for treating diseases that involve interactions between T and B
 PT cells, e.g. graft rejection or tumours
 XX
 XX Example 7; Fig 5a; 87pp; English.
 XX
 CC This sequence encodes a primatized form of the antibody 16C10 light chain
 CC from macaque. This sequence is used in a method which studies new
 CC monoclonal antibodies (Mab's) that bind selectively to B7.1 (CD80) or to
 CC B7.2 (CD86) antigens and inhibits binding of these antigens to CD28. Such
 CC Mab's are specific immunosuppressants for treatment of diseases involving
 CC T cell/B cell interactions, particularly autoimmune disease, specifically
 CC idiopathic thrombocytopenia purpura, systemic lupus erythematosus, type
 CC I diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic anaemia,
 CC inflammatory bowel disease, allergy and multiple sclerosis, graft vs.
 CC host diseases, B cell lymphoma, infections (including by human immune
 CC deficiency virus) or inflammatory disease and tumours. Optionally the
 CC Mab can be conjugated to a drug or toxin. Mab's, or their fragments, can
 CC also be used as imaging agents and as vaccines or immunogens to develop
 CC anti-idiotypic reagents. Mab's are optionally combined with other proteins
 CC or small molecule immunosuppressants. Blocking B7/CD28 interactions
 CC induces long-term, antigen-specific immunosuppression, i.e. it inhibits
 CC production of interleukin-2 (IL-2), T cell proliferation and
 CC antigen-specific immunoglobulin G (IgG) responses.
 XX
 XX Sequence 711 BP; 160 A; 226 C; 193 G; 132 T; 0 other;
 SQ

Query Match 100.0%; Score 711; DB 19; Length 711;
 Best Local Similarity 100.0%; Pred. No. 8.6e-172;
 Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGGTCCCGCTCAGCTCTGGGGCTCTGGCTCTGGCTCCCGAGTGCACGATGT 60
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 DB 61 GAGTCTGTCTGACACAGCGCGCTCAGTGTCTGGGGCCCGAGGAGAGGTCCACATC 120
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 DB 241 GACCGATTCTGTGGTCCAAAGTCTGTGACCGGGCCCTCCCTGGCCATCATCTGGTCCAG 300
 QY 301 ACTGAGGATGAGCTGATTATTACTGCCAGTCTTATGACAGAGCTGAATCTCAGGTA 360
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 QY 361 TTCGAGGAGGAGACCGGGTCCAGCTCTAGTTCAGCCCAAGGCTGCCCTCCGTCACCT 420
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 DB 481 AGTGACTTCTACCCGGGACCGTGACAGTGGCTTGAAGGAGATAGAGCCCGTCAAG 540

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 QY 601 TACCTGAGCTGACCGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTCAAG 660
 DB 601 TACCTGAGCTGACCGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTCAAG 660
 QY 661 CATGAAGGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 711
 DB 661 CATGAAGGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 711

RESULT 2
 AAS17246
 ID AAS17246 standard; DNA; 711 BP.
 XX AAS17246;
 AC AAS17246;
 DT 12-MAR-2002 (first entry)
 XX DNA sequence of a primatized form of the light chain of 16C10 antibody.
 DE Human; macaque monkey; light chain; primatized antibody; 16C10 antibody;
 XX neuroprotective; apoptosis inducer; allergy; CD28 receptor antagonist;
 KW B7.1 antigen; CD80; B7.2 antigen; CD86; B cell cancer; metastasis;
 KW tumour; B cell lymphoma; B cell leukaemia; autoimmune disease;
 KW graft-vs-host disease; immunosuppression; organ rejection;
 KW interleukin-2; IL-2; mutant; ds.
 XX Chimeric - Homo sapiens.
 OS Chimeric - Macaca sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH 1..711
 FT /*tag= a
 FT /product= "Light chain of 16C10 antibody"
 XX WO200189567-A1.
 XX 29-NOV-2001.
 XX 22-MAY-2001; 2001WO-US16364.
 XX 22-MAY-2000; 2000US-0576424.
 XX (IDEC-) IDEC PHARM CORP.
 XX Anderson DR, Hanna N, Brams P;
 XX WPI; 2002-089995/12.
 DR P-PSDB; AAU11645.
 XX
 PT Use of monoclonal antibody which specifically binds to B7.1 antigen
 PT CD80 and/or B7.2 antigen CD86 for inducing apoptosis of B7+ cells,
 PT treating cancer, graft-vs-host disease and autoimmune disease such as
 PT allergy
 XX
 PS Example 8; Fig 5a; 89pp; English.
 XX
 CC The present invention relates to a new use of a monoclonal antibody
 CC which specifically binds to B7.1 antigen (CD80) and/or B7.2 antigen
 CC (CD86) for inducing the apoptosis of B7+ cells. The invention is
 CC useful for treating diseases such as B cell cancer, lymphoma, a
 CC cancer where B cells promote the growth and/or metastasis of tumours,
 CC B cell lymphoma, B cell leukaemia, and autoimmune diseases such as
 CC idiopathic thrombocytopenia purpura, systemic lupus, erythematosus,
 CC type 1 diabetes mellitus, rheumatoid arthritis, psoriasis, aplastic
 CC anaemia, inflammatory bile disease, allergy, multiple sclerosis
 CC or graft-vs-host disease. The antibody is useful for immunosuppression
 CC in a human or animal and for treating or preventing resistance to or

QY 361 TTCGAGGAGGACCCGGCTGACCGTCTTAGGTACGCCAAGGCTCCCCCTCGGTCACT 420
Db 361 TTCGAGGAGGACCCGGCTGACCGTCTTAGGTACGCCAAGGCTCCCCCTCGGTCACT 420
QY 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCAACAAGGCCACACATGGTGTCTCATA 480
Db 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCAACAAGGCCACACATGGTGTCTCATA 480
QY 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGCGCAGATAGCAGCCCGTCAAG 540
Db 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGCGCAGATAGCAGCCCGTCAAG 540
QY 541 GCGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAGTACGCGGCCAGCAGC 600
Db 541 GCGGAGTGGAGACCAACACACCTCCAAACAAAGCAACAAGTACGCGGCCAGCAGC 600
QY 601 TACCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTCAGC 660
Db 601 TACCTGAGCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTCAGC 660
QY 661 CATGAAGGAGCAGCCGTGAGAGACAGTGGCCCTTACAGATGTTTCATGA 711
Db 661 CATGAAGGAGCAGCCGTGAGAGACAGTGGCCCTTACAGATGTTTCATGA 711

RESULT 4

ID AAC66525 standard; cDNA; 935 BP.
XX AAC66525;
XX 15-FEB-2001 (first entry)
XX Human immune system associated protein HISAP-7 coding sequence.
XX Human; immune system associated protein; HISAP-7; immune disorder;
KW infection; autoimmune disease; cancer; ss.
XX Homo sapiens.
XX US6135941-A.
XX 24-OCT-2000.
XX 27-MAR-1998; 98US-0049672.
XX 27-MAR-1998; 98US-0049672.
XX (INCY-) INCYTE PHARM INC.
XX Tang YT, Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR;
PI Hillman JL, Au-Young J;
DR WPI; 2001-030926/04.
DR P-PSDB; AAB36209.

XX New human immune system associated proteins (HISAP) and polynucleotides
PT encoding the HISAP, useful for diagnosing, treating or preventing
PT immune or cell proliferative disorders or infections
XX Claim 3; Column 83-84; 54pp; English.
XX The present invention provides the coding and protein sequences for a
CC number of human immune system associated proteins (HISAPs). These can be
CC used in the diagnosis and treatment of various autoimmune disorders,
CC infections and cell proliferation diseases. The diseases include AIDS,
CC adult respiratory distress syndrome, anaemia, asthma, atherosclerosis,
CC Crohn's disease, irritable bowel syndrome, multiple sclerosis, myasthenia
CC gravis, osteoarthritis, rheumatoid arthritis, scleroderma, systemic lupus
CC erythematosus, arteriosclerosis, cirrhosis and cancer.
XX Sequence 935 BP; 216 A; 299 C; 248 G; 172 T; 0 other;

Query Match 81.9%; Score 582.6; DB 22; Length 935;
Best Local Similarity 89.8%; Pred. No. 5.2e-139;
Matches 637; Conservative 0; Mismatches 69; Indels 3; Gaps 1;
QY 4 AGGGTCCCGGCTCAGCTCCTGGGGCTCCTGCTGCTCTGGCTCCAGGTGACGATGTGAG 63
Db 74 ATGGCTCGGTCTCCTCTCCTCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCT 133
QY 64 TCTGTCTCTGACACACGCGCCCTCAGTGTCTGGGGCCCGCAGGCGCAAGGTACCATCTCG 123
Db 134 TCTGTCTCTGACACGCGCCCTCAGTGTCTGGGGCCCGCAGGCGCAAGGTACCATCTCC 193
QY 124 TGCAGTGGGAGCACCTCCCAACATTGG---AGGTATATGATCTACATTTGTATCCAGAGCTC 180
Db 194 TGCAGTGGGAGCACCTCCCAACATTGG---AGGTATATGATCTACATTTGTATCCAGAGCTT 253
QY 181 CCAGGAACGCGCCCGCAAACTCCTCATCTATGACATTAACAAGCGCACCTCTAGGAATTTCT 240
Db 254 CCAGGAACGCGCCCGCAAACTCCTCATCTATGATGTAGTAAATCGGCCCTCAGGGGTCTCCT 313
QY 241 GACGATTTCTCTGGCTCCCAAGTCTGGTACCGCGGCTCCCTGGCCCATCACTGGGCTCCAG 300
Db 314 GACGATTTCTCTGGCTCCCAAGTCTGGTACCGCGGCTCCCTGGCCCATCACTGGGCTCCAG 373
QY 301 ACTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCTCTGAAATGCTCAGGTA 360
Db 374 GCTGAGGATGAGGCTGATTATTACTGCCAGTCTCTATGACAGCAGCTCTGAGTGTGTA 433
QY 361 TTCGAGGAGGACCCGGCTGACCGTCTAGGTGACGCCAAGGTGCCCCCTCGGTCACT 420
Db 434 TTCGAGGAGGACCCGGCTGACCGTCTAGGTGACGCCAAGGTGCCCCCTCGGTCACT 493
QY 421 CTGTTCGCGCCCTCTCTGAGGAGCTTCAAGCCACAGGCGCCACACTGGTGTCTCATA 480
Db 494 CTGTTCGCGCCCTCTCTGAGGAGCTTCAAGCCACAGGCGCCACACTGGTGTCTCATA 553
QY 481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGAGGAGTACAGAGTCCAGTCAAG 540
Db 554 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCTTGAAGGAGGAGTACAGAGTCCAGTCAAG 613
QY 541 GCGGAGTGGAGACCAACACCCCTCCAAACAAAGCAACAAGTACGCGGCCAGCAGC 600
Db 614 GCGGAGTGGAGACCAACACCCCTCCAAACAAAGCAACAAGTACGCGGCCAGCAGC 673
QY 601 TACCTGAGCCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTCAGC 660
Db 674 TACCTGAGCCTGACGCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTCAGC 733
QY 661 CATGAAGGAGCAGCCGTGAGAGACAGTGGCCCTTACAGATGTTTCAT 709
Db 734 CATGAAGGAGCAGCCGTGAGAGACAGTGGCCCTTACAGATGTTTCAT 782

RESULT 5

AAQ03609
ID AAQ03609 standard; cDNA; 884 BP.
XX AAQ03609;
AC AAQ03609;
XX 06-AUG-1989 (first entry)
XX Sequence encoding 4G12 monoclonal antibody (Mab) L chain.
XX 4G12 Mab; human lung cancer; oesophageal carcinoma; ss.
XX Synthetic.
XX Location/Qualifiers
XX Key 25..729
XX CDS /*tag= a
XX FT /product=4G12 L
XX FT 25..375
XX FT misc_feature
XX FT /*tag= b

```
FT misc_feature /label=v region
FT 376..414 /*tag= c
FT /label=j region
FT 415..729 /*tag= d
FT /label=c region
FT 835..840 /*tag= e
FT /number=1
FT 856..861 /*tag= f
FT /number=2
XX
XX JP02046289-A.
XX
XX 15-FEB-1990.
XX
XX 05-AUG-1988; 88JP-0196647.
XX
XX 05-AUG-1988; 88JP-0196647.
XX
XX (YOSH ) YOSHITOMI PHARM. IND. KK.
XX
XX WPI; 1990-094983/13.
XX P-PSDB: AAR05555.
XX
XX DNA base sequence coding for 4G12 monoclonal antibody - which reacts
XX specifically with human lung cancer and oesophageal carcinoma.
XX
XX Disclosure; Page 549; 9pp; Japanese.
XX
XX Sequence is cloned and synthetic DNA/RNA of human Ab L chain C regions
XX is used as probe to obtain sequences coding for 4G12 Mab.
XX See also AAQ03607-Q03610.
XX
XX Sequence 884 BP; 219 A; 286 C; 212 G; 166 T; 1 other;
XX
XX Query Match 80.4%; Score 571.4; DB 11; Length 884;
XX Best Local Similarity 87.9%; Pred. No. 3.7e-136;
XX Matches 623; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
XX
QY 1 ATGAGGTCCTCCGCTCAGCTCTCTGGGCTCTCTGCTCTGCTCTCCAGTGCAGATG 60
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 61 GAGTCGTCTGCACAGCGCCCTCAGTGTCTGGGCCCCAGGCGAGAGGTCCACATC 120
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 82 CAGTCGTGTGACGAGCGCCCTCAGTGTCTGGGCCCCAGGCGAGAGGTCCACATC 141
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 TCGTCACCTGGGAGCACCCTCCAACTTGGAGGTATGATCTACATTTGGTACCAGCAGCTC 180
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 142 TCTGCTCTGGAGGAGCTCCACATTTGGAGTATATGATCTCTGTTACGAGCTC 201
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 CCAGGAACGGCCCCAACTCTCTATGATTAATTAACAGCACCTCCAGAAATTTCT 240
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 202 CCAGGAACAGCCCCAACTCTCTATGATTAATTAACAGCACCTCCAGAAATTTCT 261
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 GACCGATTTCTGGTCTCAAGTCTGTACCGGCTCTCTGGCCATCATCTGGTCTCAG 300
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 262 GACCGATTTCTGGTCTCAAGTCTGTACCGGCTCTCTGGCCATCATCTGGTCTCAG 321
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 ACTGAGGATGAGCTGATTTACTGCCAGTCTATGACAGCAGCTGATGCTCAGGTA 360
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 322 ACTGGGACAGGCCGATTTACTCGGAACATGGGATAGCAGCTGATGCTGGGTA 381
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 361 TTGCGAGGAGGACCGGCTGACCGTCTTAGTTCAGGCCCAAGCTGCCCTCGTCACT 420
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 382 TTGCGGAGGAGGACCAAGCTGACCGTCTTAGTTCAGGCCCAAGCTGCCCTCGTCACT 441
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGTGTGTCTATA 480
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 442 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGTGTGTCTATA 501
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

481 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCTGGAAGGAGGAGATAGCAGCCCCGTCAAG 540
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
502 AGTGACTTCTACCCGGGAGCCGTGACAGTGGCTGGAAGGAGGAGATAGCAGCCCCGTCAAG 561
QY 541 GCGGAGTGGAGACCAACACACACCTCCAAACAAAGCAACAACAGTACGCGGCCAGCAGC 600
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
562 GCGGAGTGGAGACCAACACACACCTCCAAACAAAGCAACAACAGTACGCGGCCAGCAGC 621
QY 601 TACCTGAGCCTGAGCCCTGAGCAGTGGAGAGTCCCAAGAGTACAGCTGCCAGGTCAAG 660
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
622 TATCTGAGCCTGAGCCCTGAGCAGTGGAGTCCCAAGAGTACAGCTGCCAGGTCAAG 681
QY 661 CATGAAGGAGGAGCCGTGGAGAGACAGTGGCCCTTACAGATGTTTCA 709
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
682 CATGAAGGAGGAGCCGTGGAGAGACAGTGGCCCTTACAGATGTTTCA 730

RESULT 6
AAC84209
ID AAC84209 standard; DNA; 762 BP.
XX
XX AAC84209;
XX
XX 19-MAR-2001 (first entry)
XX
XX Plasmid Glambda-1Bpcn DNA sequence.
XX
XX Monoclonal antibody; F protein; respiratory syncytial virus; RSV;
XX Glambda-1; human; virucide; RSV propagation; ds.
XX
XX Homo sapiens.
XX
XX WO200069462-A1.
XX
XX 23-NOV-2000.
XX
XX 18-MAY-2000; 2000WO-US13694.
XX
XX 18-MAY-1999; 99US-0134702.
XX
XX (SMK ) SMITHKLINE BEECHAM CORP.
XX
XX Gross MS, Sweet RW, Taylor G;
XX WPI; 2001-024947/03.
XX
XX Human monoclonal antibody and functional fragments, useful for
XX therapeutic and/or prophylactic treatment of respiratory syncytial
XX virus infection, is specifically reactive with the F protein epitope of
XX the virus -
XX
XX Claim 3, 6; Fig 11; 102pp; English.
XX
XX The invention provides a human monoclonal antibody (I) and its functional
XX fragments specifically reactive with an F protein epitope of respiratory
XX syncytial virus (RSV), and capable of neutralizing infection by the virus
XX such as Glambda-1A or Glambda-1B. The antibody can be expressed by
XX standard recombinant methodology. (I) is useful for detecting RSV by
XX contacting a source suspected of containing RSV with (I) and determining
XX whether (I) binds to the source. (I) is also useful for providing passive
XX immunotherapy prophylactically, to RSV disease in a human. (I) is useful
XX for therapeutic and/or prophylactic treatment of RSV infection in human
XX patients, particularly infants and young children. (I) is also useful
XX as a diagnostic reagent for the determination of RSV mediated disorders
XX or for tracking progress of treatment of the disorders. The present
XX sequence represents the continuous DNA sequence of the coding region of
XX the light chain of plasmid Glambda-1Bpcn.
XX
XX Sequence 762 BP; 174 A; 241 C; 195 G; 152 T; 0 other;
XX
XX Query Match 79.5%; Score 565.2; DB 22; Length 762;
XX Best Local Similarity 91.6%; Pred. No. 1.4e-134;
```


Db 1592 AGTACGGCCAGCAGCTATCTGAGCCTGACGCTGAGCAGTGGAGTCCCAAGAAGGT 1651
Qy 644 ACAGCTGCCAGTCCAGCATGAAGGAGCACCCTGGAGAGACAGTGGCCCTTACAGAAT 703
Db 1652 ACAGCTGCCAGTCCAGCATGAAGGAGCACCCTGGAGAGACAGTGGCCCTTACAGAAT 1711
Qy 704 GTTCAT 709
Db 1712 GTTCAT 1717

RESULT 8

AA06953
ID AAX06953 standard; DNA; 768 BP.

AC AAX06953;

DT 10-MAY-1999 (first entry)

XX Monoclonal antibody 4B5 light chain variable region DNA.

XX Antigen binding fragment 4B5; monoclonal antibody; cancer;
KW neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma;
KW sarcoma; lung carcinoma; metastasis; anti-idiotypic antibody;
KW GD2 antigen; human; ds.

XX Homo sapiens.

OS
FH Key Location/Qualifiers
FT CDS 19..726
FT /*tag= a

PN WO9902545-A2.

XX 21-JAN-1999.

PF 08-JUL-1998; 98WO-IB01046.

PR 08-JUL-1997; 97US-0051945.

XX (NOVO-) NOVOPHARM BIOTECH INC.

XX Dan MD;

PI WPI; 1999-120769/10.

DR P-PSDB; AAW88465.

XX New antibody 4B5 polynucleotides and polypeptides - used to develop
PT products for the diagnosis and treatment of cancers and for
PT prophylactic therapy to reduce risk of recurrence

XX Claim 4; Page 80; 83pp; English.

XX This is the DNA sequence of a polynucleotide that encodes the light
CC chain variable region (see AAW88465) of the recombinant human
CC monoclonal antibody (WAB) 4B5. 4B5 recognises antibodies specific
CC for GD2 antigen antibodies. Antibodies specific for GD2 recognise
CC various cancers including glioblastoma, neuroblastoma, malignant
CC and/or metastatic melanoma, breast adenocarcinoma, lung
CC adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
CC prostate adenocarcinoma. The invention encompasses 4B5 derivatives
CC with immunologic specificity for antibodies specific for GD2. These
CC derivatives, or antigen binding fragments, comprise regions of the
CC 4B5 VDJ junction and regions spanning the 4B5 CDRs. Other
CC derivatives include Fab, Fab', scFv and isolated heavy and
CC light chains. Polynucleotide fragments (see AAX06951-54), both
CC coding and complementary strands, encoding 4B5 antibody V regions
CC are also provided, as well as therapeutic plasmids and vectors,
CC including vaccinia virus vectors, comprising these polynucleotides.
CC 4B5 has been shown to mimic GD2, and is particularly useful in
CC generating a host immune response to cancer. Products of the
CC invention can be used in the detection and treatment of e.g.

CC astrocytoma, oligodendroglioma, ependymoma, medulloblastoma,
CC primitive neural ectodermal tumour (PNET), pancreatic ductal
CC adenocarcinoma, small and large cell lung adenocarcinomas,
CC squamous cell carcinoma, bronchoalveolar carcinoma, epithelial
CC adenocarcinoma, and liver metastases, hepatoma, cholangiocarcinoma,
CC breast tumours such as ductal and lobular adenocarcinoma, squamous
CC and adenocarcinomas of the uterine cervix, uterine and ovarian
CC epithelial carcinoma, prostatic adenocarcinoma, transitional
CC squamous cell carcinoma of the bladder, B and T cell lymphoma
CC (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
CC malignant melanoma, soft tissue sarcoma and leiomyosarcoma.
XX
SQ Sequence 768 BP; 169 A; 256 C; 202 G; 141 T; 0 other;

Query Match 77.7%; Score 552.6; DB 20; Length 768;

Best Local Similarity 89.6%; Pred. No. 2.2e-131;

Matches 594; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 47 CAGGTGCAGATGTGAGTCTCTCTGACACAGCCGCCCTCAGTCTCTGGGGCCCCAGGCG 106

Db 62 CAGGGTCTCTGGGCCAGTCTGTGTGACTGACGCCACCTCAGCGCTCTGGGACCCCGGGC 121

Qy 107 AGAAGGTCAACATCTCTGTCGTCAGTGGAGCACCTCCAAACATTGGAGTTATGATCTACATT 166

Db 122 AGAGGTGACCATCTCTTGTCTGGAAGCACTCCAAACATCGGAAGTAGACTGTAACT 181

Qy 167 GGTACACAGCAGCTCCAGGAAGCGGCCCAAACTCTCATCTATGACATTAACAAGCGAC 226

Db 182 GGTACACAGCACTCCAGGAAGCGGCCCAAACTCTCATCTATGATTAATAATACGCGC 241

Qy 227 CCTCAGGAATTTCTGACCGATTTCTTGGTCTCAAGTCTGGTACCGGGCTCTCCCTGGCCA 286

Db 242 CCTCAGGGGTCTCTGACCGATTTCTTGGTCTCAAGTCTGGTACCGGGCTCTCCCTGGCCA 301

Qy 287 TCACCTGGGCTCCAGACTGAGGATGAGTCTGATTTACTTGCAGTCTCTATGACAGCGC 346

Db 302 TCAGTGGGCTCCAGTCTGAGGATGAGTCTGATTTACTTGCAGTCTCTATGACAGCGC 361

Qy 347 TGAATGCTCAGGTATTCGGAGGAGGAGCCCGGCTGACCGTCTCTAGGTCTAGCCCAAGGCTG 406

Db 362 TGAATGCTGAGTCTGAGTCTGAGGAGGAGCCCAAGTCTGAGTCTAGCCCAAGGCTG 421

Qy 407 CCCCCCTGGTCACTCTGTTTCCCGCTCTCTCTGAGGAGTCTCAAGCAACAAGGCCACAC 466

Db 422 CCCCCCTGGTCACTCTGTTTCCCGCTCTCTCTGAGGAGTCTCAAGCAACAAGGCCACAC 481

Qy 467 TGGTGTGTCTCATTAAGTCACTTCTACCGGGAGCGTGACAGTGGCTTGGAGGAGGAGATA 526

Db 482 TGGTGTGTCTCATTAAGTCACTTCTACCGGGAGCGTGACAGTGGCTTGGAGGAGGAGATA 541

Qy 527 GCAGCCCCGTCAAGCGGGAGTGGAGACCAACACACCTCTCCAAACAAAGCAACAAGT 586

Db 542 GCAGCCCCGTCAAGCGGGAGTGGAGACCAACACACCTCTCCAAACAAAGCAACAAGT 601

Qy 587 AGCGGGCAGCAGTCTGAGTCTGAGCCTGAGCCTGAGCAGTGGAGTCCCAAGAAGTACA 646

Db 602 AGCGGGCAGCAGTCTGAGTCTGAGCCTGAGCCTGAGCAGTGGAGTCCCAAGAAGTACA 661

Qy 647 GGTGCCAGGTCAAGTCTGAGGAGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGAATGTT 706

Db 662 GGTGCCAGGTCAAGTCTGAGGAGGAGCAGCGTGGAGAGACAGTGGCCCTTACAGAATGTT 721

Qy 707 CAT 709

Db 722 CAT 724

RESULT 9

AA06954/c

ID AAX06954 standard; DNA; 768 BP.

XX AAX06954;

XX

DT 10-MAY-1999 (first entry)
 XX Monoclonal antibody 4B5 light chain variable region DNA.
 XX
 KW Antigen binding fragment 4B5; monoclonal antibody; cancer;
 KW neoplasm; diagnosis; therapy; melanoma; neuroblastoma; glioma;
 KW sarcoma; lung carcinoma; metastasis; anti-idiotype antibody;
 KW GD2 antigen; human; ds.
 XX
 XX Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS complement (43..750)
 FT /*tag= a
 XX
 XX W09902545-A2.
 XX
 XX 21-JAN-1999.
 XX
 XX 08-JUL-1998; 98WO-IB01046.
 XX
 XX 08-JUL-1997; 97US-0051945.
 XX
 XX (NOVO-) NOVOPHARM BIOTECH INC.
 XX
 XX Dan MD;
 XX
 XX WPI; 1999-120769/10.
 XX
 XX P-PSDB; AAW88465.
 XX
 XX New antibody 4B5 polynucleotides and polypeptides - used to develop
 XX products for the diagnosis and treatment of cancers and for
 XX prophylactic therapy to reduce risk of recurrence
 XX
 XX Claim 6; Page 80; 83pp; English.
 XX
 XX This is the complementary strand of a DNA sequence (see also
 XX AAX06953) that encodes the light chain variable region (see AAW88465)
 XX of the recombinant human monoclonal antibody (MAB) 4B5. 4B5
 XX recognises antibodies specific for GD2 antigen antibodies. Such
 XX antibodies recognise various cancers including glioblastoma,
 XX neuroblastoma, malignant and/or metastatic melanoma, breast
 XX adenocarcinoma, lung adenocarcinoma, small cell lung carcinoma,
 XX colon adenocarcinoma and prostate adenocarcinoma. The invention
 XX encompasses 4B5 derivatives with immunologic specificity for
 XX antibodies specific for GD2. These derivatives, or antigen binding
 XX fragments, may comprise regions of the 4B5 VDJ junction and regions
 XX spanning the 4B5 CDRs. Other derivatives include Fab, Fab', J2,
 XX Fab', scFv and isolated heavy and light chains. Polynucleotide
 XX fragments (see AAX06951-54), both coding and complementary strands,
 XX encoding 4B5 antibody V regions are also provided, as well as
 XX therapeutic plasmids and vectors, including vaccinia virus vectors,
 XX comprising these polynucleotides. 4B5 mimics GD2, and is useful in
 XX generating a host immune response to cancer. Products of the
 XX invention can be used in the detection and treatment of e.g.
 XX astrocytoma, oligodendroglioma, ependymoma, medulloblastoma,
 XX primitive neural ectodermal tumour (PNET), pancreatic ductal
 XX adenocarcinoma, small and large cell lung adenocarcinomas,
 XX squamous cell carcinoma, bronchoalveolar carcinoma, epithelial
 XX adenocarcinoma, and liver metastases, hepatoma, cholangiocarcinoma,
 XX breast tumours such as ductal and lobular adenocarcinoma, squamous
 XX and adenocarcinomas of the uterine cervix, uterine and ovarian
 XX epithelial carcinoma, prostatic adenocarcinoma, transitional
 XX squamous cell carcinoma of the bladder, B and T cell lymphoma
 XX (nodular and diffuse), plasmacytoma, acute and chronic leukemia,
 XX malignant melanoma, soft tissue sarcoma and leiomyosarcoma.
 XX
 XX Sequence 768 BP; 141 A; 202 C; 256 G; 169 T; 0 other;
 XX
 XX Query Match 77.7%; Score 552.6; DB 20; Length 768;
 XX Best Local Similarity 89.6%; Pred. No. 2.2e-131;
 XX Matches 594, Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 47 CAGGTGCACGATGTGAGTCTGTCTGTGACACAGCCGCCCTCAGTGTCTGGGGCCCCAGGGC 106
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 648
 QY 107 AGAAGGTACCATCTCTCGTGCACCTGGGAGCAGCTCCAAATTCATGAGGTTATGATCTACATT 166
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 588
 QY 167 GGTACACAGCAGTCCACAGGAACGGCCCAAACTCTCATCTATGACATTAAACAGCGAC 226
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 528
 QY 227 CCTCAGGAATTTCTGACCGATTCTCTGGCTCCAACTCTGGTACCGCGCTCTCCCTGGCCA 286
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 468
 QY 287 TCACCTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCTTATGACAGAGCC 346
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 408
 QY 347 TGAATGCTCAGTATTTCGAGGAGGACCCGCTGACCGTCTCTAGTCTCAGCCCAAGGCTG 406
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 348
 QY 407 CCCCCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAGGCCACAC 466
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 288
 QY 467 TGGTGTGCTCATAGTCACTTCTACCCGGGAGCGCTGACAGTGGCCCTGGAGGAGGAGATA 526
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 228
 QY 527 GCAGCCCCGTCAAGCGGGAGTGGAGACCAACACACCTCCAAACAAAGCAACACCAAGT 586
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 168
 QY 587 ACGGGCCAGCAGCTACTGTAGCCCTGACGCTGAGCAGTGGAGTCCACAGAACTACA 646
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 108
 QY 647 GCTGCCAGGTACCGATGAAGGAGCACCCTGGGAGAACACAGTGGCCCTTACAGATGTT 706
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 48
 QY 707 CAT 709
 DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 DB 47 CAT. 45

RESULT 10
 AAO49835
 ID AAO49835 standard; cDNA; 654 BP.
 XX AAO49835;
 XX
 XX 27-APR-1994 (first entry)
 XX
 XX Anti-HIV-1 recombinant antibody 447-52D light chain coding sequence.
 XX
 XX Human Immunodeficiency Virus; antigen; ELISA; recombinant antibody;
 XX HIV-neutralising monoclonal antibody; immunoglobulin; AIDS;
 XX acquired immune deficiency syndrome; chimeric antibody;
 XX surface glycoprotein gp120; V3 loop; ss.
 XX
 XX Homo sapiens.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 1..654
 FT /*tag= a
 FT /note= "encodes recombinantly modified 447-52D
 FT light chain"
 XX
 XX W09319785-A.

XX 14-OCT-1993.
XX 23-MAR-1993; 93WO-US02629.
XX 01-APR-1992; 92US-0861701.
XX (MERI) MERCK & CO INC.
XX (JOHN/) JOHNSON L S.
XX (PFAR/) PFARR D S.
XX Conley AJ, Emimi EA, Johnson LS, Mark GE, Pfarr DS;
XX WPI; 1993-336600/42.
XX P-PSDB; AAR42163.
XX New recombinant human antibody - with HIV neutralising activity
XX against at least two isolates, useful for preventing or treating
XX infection in diagnosis, etc.
XX Example 9; Fig 2B; 154pp; English.
XX EBV-transformed cell lines and mouse-human heterohybridomas
XX producing human Wabs specific for the gp120 V3 loop of HIV-1 MN
XX isolate were obtained. Wab 447-52D was found to recognise the
XX tetrapeptide motif GPR, i.e. the Principal Neutralising
XX Determinant common to the V3 loop of different HIV isolates.
XX A recombinant Ab was produced in which the L chain V region was
XX derived from 447-52D and to which a signal sequence and a L chain
XX intronic sequence are appended, fused to a fragment contg. a short
XX intronic segment of the human lambda 2 C region and the human
XX lambda 2 constant encoding domain.
XX Sequence 654 BP; 156 A; 199 C; 178 G; 121 T; 0 other;
SQ

Query Match 76.9%; Score 547; DB 14; Length 654;
Best Local Similarity 91.1%; Pred. No. 5.8e-130;
Matches 593; Conservative 0; Mismatches 55; Indels 3; Gaps 1;
XX 62 AGTCGTCTCTACACAGCGCCCTCAGTGTCTGGGCCCCCAGGAGGTGACCATCT 121
DB 2 AGTCGTGTGACGAGCGCCCTCAGTGTCTGGGCCCCCAGGAGGTGACCATCT 61
XX 122 COTGCACTGGGAGCCTCCAACTGGAGGTATGATCTACATGTTACGAGCTCC 181
DB 62 CCGTCTCTGGAAGCAGCTCCAACTGGGAATAATATGTTGTTACGAGCTTC 121
XX 182 CAGGAACGGCCCCCAACTCCTCATCTATGACATTAACAGGACCTCAGGAATTCG 241
DB 122 CAGGAACAGCCCCCAACTCCTCATTTATGGCAATAATAAGGACCTCAGGATTCCTG 181
XX 242 ACCGATTTCTTGCTCCAGTCTGGTACCGCGCCCTCCCTGCGCATCACTGGGCTCCAGA 301
DB 182 ACCGATTTCTTGCTCCAGTCTGGCAGCTGACGACCTGGGCACTACCGGACTCCAGA 241
XX 302 CTGAGGATGAGGTGATTTACTGTCAGTCTCTATGACAGCAGCTGGAATGCTCA---GG 358
DB 242 CTGGGAGCAGGCGCGATTTATTTCTGCGCAACATGGATAGCGCCTGAGTGTGATTGG 301
XX 359 TATTCGAGGAGGAGCCCGGTGACGCTGAGTTCAGGTCAGCCCAAGGCTGCCCTCGGTCA 418
DB 302 TGTTCGGCGAGGAGCAAGCTGACGCTCTTAAGTCAGCCCAAGGCTGCCCTCGGTCA 361
XX 419 CTCTGTTCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGGTGTCTCA 478
DB 362 CTCTGTTCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCCACACTGGTGTCTCA 421
XX 479 TAAGTGACTTCTACCGGAGCGGTGACAGTGCGCTTGGAGGAGCAGATAGCAGCCCGTCA 538
DB 422 TAAGTGACTTCTACCGGAGCGGTGACAGTGCGCTTGGAGGAGCAGATAGCAGCCCGTCA 481
XX 539 AGCGGGAGTGAGAGCACCAACCTCCAAACAAAGCAACAAAGTACGGCGGCAGCA 598
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Db 482 AGCGGGAGTGGAGACCAACACACCTCCAAACAAGCAACAAGTACGGCGCAGCA 541
QY 599 GCTACTGAGCTGACGCTGAGCAGTGAAGTCCACAGAGCTACAGCTCCAGGTCA 658
Db 542 GCTATCTGAGCTGACGCTGAGCAGTGAAGTCCACAGAGCTACAGCTCCAGGTCA 601
QY 659 CGCATGAAGGGAGCACCGCTGGAGAGACAGTGGCCCTACAGAAATGTTTCAT 709
Db 602 CGCATGAAGGGAGCACCGCTGGAGAGACAGTGGCCCTACAGAAATGTTTCAT 652
RESULT 11
AAS87270
ID AAS87270 standard; cDNA; 810 BP.
XX
AC AAS87270;
XX
DT 13-FEB-2002 (first entry)
XX
DE DNA encoding novel human diagnostic protein #23074.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX P-PSDB; ABG23083.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 1; SEQ ID No 23074; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 810 BP; 176 A; 275 C; 211 G; 148 T; 0 other;

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 17:51:01 ; Search time 93.7363 Seconds
(without alignments)
10227.493 Million cell updates/sec

Title: US-09-576-424-9
Perfect score: 711
Sequence: 1 atgggggtcccgctcagct.....ccctacagaatgtcatga 711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 845702 seqs, 674182571 residues

Total number of hits satisfying chosen parameters: 1691404

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	711	9	US-10-124-905-9
2	711	100.0	711	9	US-09-948-4298-9
3	711	100.0	711	9	US-10-073-138-5
4	552.6	77.7	768	10	US-09-747-669-4
5	552.6	77.7	768	10	US-09-747-669-5
6	552.6	77.7	848	9	US-10-158-646-70
7	550.6	77.4	888	9	US-10-158-646-71
8	540.2	76.0	705	9	US-10-124-905-1
9	540.2	76.0	705	9	US-09-948-4298-1
10	540.2	76.0	705	9	US-10-073-138-1
11	534.8	75.2	2112	9	US-10-001-857-108
12	532.2	74.9	915	10	US-09-954-456-788
13	532.2	74.9	915	10	US-09-880-107-3743
14	504.2	70.9	883	9	US-10-158-646-73
15	484.2	68.1	885	9	US-09-852-797-47
16	484.2	68.1	885	10	US-09-853-161-47
17	484.2	68.1	885	10	US-09-852-659A-47
18	482.6	67.9	879	9	US-09-852-797-29
19	482.6	67.9	879	10	US-09-853-161-29

20	482.6	67.9	879	10	US-09-852-659A-29
c 21	474	66.7	2667	9	US-10-158-646-76
22	468.4	65.9	702	9	US-10-211-357-5
23	457.6	64.4	960	10	US-09-925-301-582
24	456	64.1	868	10	US-09-822-849A-157
c 25	449.8	63.3	1480	9	US-09-981-353-146
26	446.8	62.8	2667	9	US-10-158-646-76
27	440.2	61.9	857	10	US-09-822-849A-158
28	429.4	60.4	846	9	US-09-981-353-55
29	422.8	59.5	938	9	US-09-828-995B-25
c 30	422.8	59.5	938	9	US-09-828-995B-27
31	422.4	59.4	830	9	US-09-981-353-42
c 32	412	57.9	928	9	US-09-852-797-46
33	412	57.9	928	10	US-09-853-161-46
c 34	412	57.9	928	10	US-09-852-659A-46
35	411.4	57.9	670	9	US-09-968-433-36
c 36	410	57.7	611	9	US-09-968-433-36
37	410	57.7	611	9	US-09-968-433-37
38	408	57.4	826	9	US-10-098-841-316
c 39	405.8	57.1	543	9	US-09-736-457-970
c 40	405.8	57.1	543	9	US-09-902-941-970
c 41	405.8	57.1	543	9	US-09-849-626-970
c 42	405.8	57.1	543	9	US-10-017-754-970
c 43	397.8	55.9	648	10	US-09-736-371B-18
44	396.6	55.8	5079	10	US-09-809-517A-41
45	394.2	55.4	1480	9	US-09-981-353-146

ALIGNMENTS

RESULT 1
US-10-124-905-9
; Sequence 9, Application US/10124905
; Patent No. US20020166136A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/124.905
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 711 base pairs

Sequence 29, Appl
Sequence 76, Appl
Sequence 5, Appl
Sequence 582, App
Sequence 157, App
Sequence 146, App
Sequence 76, Appl
Sequence 158, App
Sequence 55, Appl
Sequence 25, Appl
Sequence 27, Appl
Sequence 42, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 36, Appl
Sequence 37, Appl
Sequence 316, App
Sequence 970, App
Sequence 970, App
Sequence 970, App
Sequence 18, Appl
Sequence 41, Appl
Sequence 146, App

; TYPE: nucleic acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..711
 ; FEATURE:
 ; NAME/KEY: mat peptide
 ; LOCATION: 1..711
 ;
 ; US-10-124-905-9

Query Match 100.0%; Score 711; DB 9; Length 711;
 Best Local Similarity 100.0%; Pred. No. 7.5e-213;
 Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db |||||
 QY 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCAAGGCGAGAGGTCAACATC 120
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 QY 121 TCGTCACTGGGAGCACCTCCAACTTGGAGGTATGATCTACATTTGGTACCAGAGCTC 180
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 QY 181 CCAGAAAGCGCCCAAACTCTCTATGACATTAACAGCGACCTCAGGAATTTCT 240
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RESULT 2

US-09-948-429B-9
 ; Sequence 9, Application US/09948429B
 ; Patent No. US20020177689A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Darrell R.
 ; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
 ; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,"

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
 ; IMMUNOSUPPRESSANTS"
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 ; STREET: 699 Prince Street
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/948,429B
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/383,916
 ; FILING DATE:
 ; APPLICATION NUMBER: US 08/487,550
 ; FILING DATE: 07-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Teskin, Robin L.
 ; REGISTRATION NUMBER: 35,030
 ; REFERENCE/DOCKET NUMBER: 012712-131
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 703-836-6620
 ; TELEFAX: 703-836-2021
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 711 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..711
 ; FEATURE:
 ; NAME/KEY: mat peptide
 ; LOCATION: 1..711
 ; US-09-948-429B-9

Query Match 100.0%; Score 711; DB 9; Length 711;
 Best Local Similarity 100.0%; Pred. No. 7.5e-213;
 Matches 711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGTCCTCCGCTCAGCTCTGGGGCTCTGGCTCTGGCTCTGGCTCCAGGTGCAGATGT 60
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 QY 181 CCAGAAAGCGCCCAAACTCTCTATGACATTAACAGCGACCTCAGGAATTTCT 240
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 QY 301 ACTGAGGATGAGGCTGATTTACTTCCAGTCTTATGACAGCAGCTGAATGCTCAGGTA 360
 Db |||||
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 Db |||||

NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRADEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: CDS
LOCATION: 1..705
FEATURE:
NAME/KEY: mat peptide
LOCATION: 1..705
US-09-948-429B-1

Query Match 76.0%; Score 540.2; DB 9; Length 705;
Best Local Similarity 86.1%; Pred. No. 2.4e-159;
Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

QY 1 ATGAGGTCCTCCGCTCAGCTCTCTGGGCTCTGCTGCTCTGGCTCCAGGTGACGATGT 60
DB 1 ATGAGGTCCTCCGCTCAGCTCTCTGGGCTCTGCTGCTCTGGCTCCAGGTGACGATGT 60

QY 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCGAGGAGAGGTCCACATC 120
DB 61 GCCTATGAATGACTCAGTGTCTGGGCTCTGCTGCTCTGGCTCCAGGTGACGATC 120

QY 121 TCGTGCATCTGGAGCACCTCCAAATTTGGAGGTATGATCTACATTGGTACGAGCTC 180
DB 121 ACCTGTGGGG-----AGACAAACAGTAGAATGATGTCTGCTCCAGGTGACGAG 174

QY 181 CCAGGACGGCCCCCAAACTCTCATCTATGATTAACAGCGACCTCAGGAATTTCT 240
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QY 175 CCAGGACGGCCCCCAAACTCTCATCTATGATTAACAGCGACCTCAGGAATTTCT 234
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RESULT 10
US-10-073-138-1
Sequence 1, Application US/10073138
Publication No. US20020187146A1
GENERAL INFORMATION:
APPLICANT: ANDERSON, Darrell R.
HANNA, Nabil
BRAMS, Peter
TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING
INTERACTIONS BETWEEN CERTAIN ANTIBODIES AND THE HUMAN B7.1
AND B7.2 CO-STIMULATORY ANTIGENS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/073,138
FILING DATE: 13-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/746,361
FILING DATE: 08-NOV-1996
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-256
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 705 base pairs
TYPE: nucleic acid
STRADEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..705
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-073-138-1

Query Match 76.0%; Score 540.2; DB 9; Length 705;
Best Local Similarity 86.1%; Pred. No. 2.4e-159;
Matches 612; Conservative 0; Mismatches 93; Indels 6; Gaps 1;

QY 1 ATGAGGTCCTCCGCTCAGCTCTCTGGGCTCTGCTGCTCTGGCTCCAGGTGACGATCT 60
DB 1 ATGAGGTCCTCCGCTCAGCTCTCTGGGCTCTGCTGCTCTGGCTCCAGGTGACGATCT 60

QY 61 GAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCGAGGAGAGGTCCACATC 120
DB 61 GCCTATGAATGACTCAGTGTCTGGGCTCTGCTGCTCTGGCTCCAGGTGACGATC 120

QY 121 TCGTGCATCTGGAGCACCTCCAAATTTGGAGGTATGATCTACATTGGTACGAGCTC 180
DB 121 ACCTGTGGGG-----AGACAAACAGTAGAATGATGTCTGCTCCAGGTGACGAG 174

QY 181 CCAGGACGGCCCCCAAACTCTCATCTATGATTAACAGCGACCTCAGGAATTTCT 240
DB 181 CCAGGACGGCCCCCAAACTCTCATCTATGATTAACAGCGACCTCAGGAATTTCT 240

QY 175 CCAGGACGGCCCCCAAACTCTCATCTATGATTAACAGCGACCTCAGGAATTTCT 234
DB 175 CCAGGACGGCCCCCAAACTCTCATCTATGATTAACAGCGACCTCAGGAATTTCT 234

QY 241 GACCGATTCTCTGGCTCCAAAGTCTGTGACCGCGCCCTCCTGGCCATCACTGGGCTCCAG 300
Db 235 GAGCGATTCTCTGGCTCCAAATCAGGGAACACCGCCCACTGACCATCAACGGGTCGAG 294
QY 301 ACTGAGATGAGGCTGATTATTAAGTCCAGTCTGTGACAGCAGCCTGAAATGCTCAGGTA 360
Db 295 GCCGGGATGAGGCTGACTATTACTGTCAGGTGTGGGACAGGGCTAGTGTATCATCCGGTC 354
QY 361 TTCGAGGAGGACCGGCTGACCGTCTAGTGCAGCCCAAGGCTGCCCTCGGTCACT 420
Db 355 TTCGAGGAGGACCGGCTGACCGTCTAGTGCAGCCCAAGGCTGCCCTCGGTCACT 414
QY 421 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAAAGCCACACTGGTGTCTCATTA 480
Db 415 CTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAACAAAGCCACACTGGTGTCTCATTA 474
QY 481 AGTGACTTACCCGGGAGCGTGACAGTGGCTGGAAGGAGATGACGCCCGGTCAAG 540
Db 475 AGTGACTTACCCGGGAGCGTGACAGTGGCTGGAAGGAGATGACGCCCGGTCAAG 534
QY 541 GCGGGAGTGAGACACACACCTCCAAACAAAGCAACAAAGTACCGGGCCAGCAGC 600
Db 535 GCGGGAGTGAGACACACACCTCCAAACAAAGCAACAAAGTACCGGGCCAGCAGC 594
QY 601 TACTGAGCTGACCGCTGAGCAGTGGAGTGGAGTCCACAGAGCTTACAGTGCAGGTCAGC 660
Db 595 TACTGAGCTGACCGCTGAGCAGTGGAGTGGAGTCCACAGAGCTTACAGTGCAGGTCAGC 654
QY 661 CATGAAGGAGACCGCTGAGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 711
Db 655 CATGAAGGAGACCGCTGAGGAGAGACAGTGGCCCTTACAGATGTTTCATGA 705

RESULT 11

US-10-001-857-108
; Sequence 108, Application US/10001857
; Publication No. US20020183500A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Herve
; APPLICANT: Chen, Sei-Yu
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Lung Specific Genes and Prod
; FILE OF INVENTION: DEX-0273
; CURRENT APPLICATION NUMBER: US/10/001,857
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/252,054
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 108
; LENGTH: 2112
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (2005)..(2005)
; OTHER INFORMATION: a, c, g or t
US-10-001-857-108

Query Match 75.2%; Score 534.8; DB 9; Length 2112;
Best Local Similarity 89.4%; Pred. No. 1.5e-157;
Matches 601; Conservative 0; Mismatches 62; Indels 9; Gaps 2;
QY 44 TCCAGGTGCACGATGTAGTCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCCAG 103
Db 794 TCTAGGGTCTGGGCCAGTCTGTCTGACGAGCGCCCTCAGTGTCTGGGGCCCCAG 853
QY 104 GCGAGAGTCAACCTCTGTCGACTGGGAGCACTCCAAATTTGAG-----GTTATG 157
Db 854 GCGAGAGGTCAACCTCTCTGCACTGGGAGCAGCTCCAAATTTGAGTTATGACT 913

QY 158 ATCTACATTGGTGTACGAGCAGCTCCAGGAACGGCCCCCAAACTCCTCATCTATGACATTA 217
Db 914 ATGTACACTGGTGTACGAGCAGCTTCAGGAAACAGCCCCCAAACTCATGATTATGAGGTG 973
QY 218 ACAAGCGACCTCTCAGGAATTTCTGACCGATTTCTTGGTCTCAAGTCTGTGTACCGGGCT 277
Db 974 CTAAGCGACCTCTCAGGGGTTTCTGATCGCTTCTTGGTCTCAAGTCTGTGTGCAACAGGGCT 1033
QY 278 CCCTGGCCATCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCTTATG 337
Db 1034 CCCTGACCATCTCTGGGCTCCAGGCTGAGGACGAGGCTGATTATTACTGCTCTCATATG 1093
QY 338 ACAGCAGCCTGAACTCTCAGGTATTTCGGAGGAGGACCGGCTGACCGCTCTAGGTTCAGC 397
Db 1094 CAGGAGC---TACACTTGGGTGTTCCGGCGGAGGACCAAGCTGACCGCTCTAGGTTCAGC 1150
QY 398 CCAAGGCTGCCCTCTCGGTCACTCTGTTCCCGCCCTCTCTGAGAGGCTTCAAGCCAAACA 457
Db 1151 CCAAGGCTGCCCTCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAACA 1210
QY 458 AGGCCACACTGGTGTCTCATAGTGTACTTACCGGGAGCGCTGACAGTGGCTGGA 517
Db 1211 AGGCCACACTGGTGTCTCATAGTGTACTTACCGGGAGCGCTGACAGTGGCTGGA 1270
QY 518 AGGCAGATAGCAGCCCGCTCAAGGCGGAGTGGAGACCAACACCCCTCCAAACAAAGCA 577
Db 1271 AGGCAGATAGCAGCCCGCTCAAGGCGGAGTGGAGACCAACACCCCTCCAAACAAAGCA 1330
QY 578 ACAACAAAGTACCGGCCAGCAGCTACTGAGCCTGACCGCTGAGCAGTGGAGTCCCCACA 637
Db 1331 ACAACAAAGTACCGGCCAGCAGCTACTGAGCCTGACCGCTGAGCAGTGGAGTCCCCACA 1390
QY 638 GAGCTACAGCTGCCAGGTCAAGGAGGAGCAGCGTGGAGAGACAGTGGGCCCCCTA 697
Db 1391 AAAGCTACAGCTGCCAGGTCAAGGAGGAGCAGCGTGGAGAGACAGTGGGCCCCCTA 1450
QY 698 CAGATGTTTCAT 709
Db 1451 CAGATGTTTCAT 1462

RESULT 12

US-09-954-456-788
; Sequence 788, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
; FILE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27

; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 788
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-788

Query Match 74.9%; Score 532.2; DB 10; Length 915;
Best Local Similarity 88.8%; Pred. No. 8.1e-157;
Matches 589; Conservative 0; Mismatches 68; Indels 6; Gaps 1;
QY 47 CAGGTGCACGATGTGAGTCTGCTCTGACACAGCGCGCTCAGTGTCTGGGGCCCCAGGGC 106
Db 158 CAGGGTCTCTGGGCCAGTCTGTGCTGACTCAGCACCCTCAGCGCTCTGGAGCCCCGGGC 217
QY 107 AGAAGGTCAACATCTCGTGCACCTGGGAGCACCTCCAACTTGGAGGTATGATCTACATT 166
Db 218 AGAGGTCAACATCTCTTGTCTGGAGCGCTCCAACTCTCATCTATAGTAATATGTTAACT 277
QY 167 GTTACAGAGTCTCCAGGAAGCGCCCCAACTCTCTCATCTATGACATTAACAAGCGAC 226
Db 278 GTTACAGAGTCTCCAGGAAGCGCCCCAACTCTCTCATCTATAGTAATATGTTAACT 277
QY 227 CCTCAGGAATTTCTGACCGATTTCTGGCTCCAACTTGGGTACCGCGGCTCTCCCTGGCCA 286
Db 338 CCTCAGGGTCTCCAGGAAGCGCCCCAACTCTCTCATCTATGACATTAACAAGCGAC 337
QY 287 TCACCTGGGTCCAGACTGAGGATGAGGCTGATTATTACTATGACATTAACAAGCGAC 346
Db 398 TCAGTGGGTCTCCAGTCTGAGGATGAGGCTGATTATTACTATGACATTAACAAGCGAC 455
QY 347 TGAATGCTCAGGTATTTCCGAGGAGGAGCGCGCTGACCGCTCTAGGTGAGCCCAAGGCTG 406
Db 456 ----TACTGTGTCTTCGGGAGGAGGACCAAGCTGACCGCTCTGTCAGCCCAAGGCTG 511
QY 407 CCCCCTCGGTCACTCTGTTCCTCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCGCACAC 466
Db 512 CCCCCTCGGTCACTCTGTTCCTCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCGCACAC 571
QY 467 TGTGTGTCTCATAGTACTTCTACCCGGAGCGGTGACAGTGGGCTGGAAGGCAGATA 526
Db 572 TGTGTGTCTCATAGTACTTCTACCCGGAGCGGTGACAGTGGGCTGGAAGGCAGATA 631
QY 527 GCAGCCCGCTCAAGCGGGAGTGGAGACCAACCAACCCCTCCAAACAAAGCAACAAGT 586
Db 632 GCAGCCCGCTCAAGCGGGAGTGGAGACCAACCAACCCCTCCAAACAAAGCAACAAGT 691
QY 587 ACAGCGCCAGCAGTACCTGAGCCTGACGCTGAGCAGTGGAGTCCCAAGAGCTACA 646
Db 692 ACAGCGCCAGCAGTATCTGAGCCTGAGCAGTGGAGTCCCAAGAGCTACA 751
QY 647 GCTGCCAGGTCAAGGAGGAGGAGCGCTGAGAGGAGCAGTGGCCCTTACAGATGTT 706
Db 752 GCTGCCAGGTCAAGGAGGAGGAGCGCTGAGAGGAGCAGTGGCCCTTACAGATGTT 811
QY 707 CAT 709
Db 812 CAT 814

RESULT 13
US-09-880-107-3743
; Sequence 3743, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107

; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3743
; LENGTH: 915
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57809
US-09-880-107-3743

Query Match 74.9%; Score 532.2; DB 10; Length 915;
Best Local Similarity 88.8%; Pred. No. 8.1e-157;
Matches 589; Conservative 0; Mismatches 68; Indels 6; Gaps 1;
QY 47 CAGGTGCACGATGTGAGTCTGCTCTGACACAGCGCGCTCAGTGTCTGGGGCCCCAGGGC 106
Db 158 CAGGGTCTCTGGGCCAGTCTGTGCTGACTCAGCACCCTCAGCGCTCTGGAGCCCCGGGC 217
QY 107 AGAAGGTCAACATCTCGTGCACCTGGGAGCACCTCCAACTTGGAGGTATGATCTACATT 166
Db 218 AGAGGTCAACATCTCTTGTCTGGAGCGCTCCAACTCTCATCTATGACATTAACAAGCGAC 277
QY 167 GTTACAGAGTCTCCAGGAAGCGCCCCAACTCTCTCATCTATGACATTAACAAGCGAC 226
Db 278 GTTACAGAGTCTCCAGGAAGCGCCCCAACTCTCTCATCTATGACATTAACAAGCGAC 337
QY 227 CCTCAGGAATTTCTGACCGATTTCTGGCTCCAACTTGGGTACCGCGGCTCTCCCTGGCCA 286
Db 338 CCTCAGGGTCTCCAGGAAGCGCCCCAACTCTCTCATCTATGACATTAACAAGCGAC 397
QY 287 TCACCTGGGTCCAGACTGAGGATGAGGCTGATTATTACTATGACATTAACAAGCGAC 346
Db 398 TCAGTGGGTCTCCAGTCTGAGGATGAGGCTGATTATTACTATGACATTAACAAGCGAC 455
QY 347 TGAATGCTCAGGTATTTCCGAGGAGGAGCGCGCTGACCGCTCTAGGTGAGCCCAAGGCTG 406
Db 456 ----TACTGTGTCTTCGGGAGGAGGACCAAGCTGACCGCTCTGTCAGCCCAAGGCTG 511
QY 407 CCCCCTCGGTCACTCTGTTCCTCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCGCACAC 466
Db 512 CCCCCTCGGTCACTCTGTTCCTCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCGCACAC 571
QY 467 TGTGTGTCTCATAGTACTTCTACCCGGAGCGGTGACAGTGGGCTGGAAGGCAGATA 526
Db 572 TGTGTGTCTCATAGTACTTCTACCCGGAGCGGTGACAGTGGGCTGGAAGGCAGATA 631
QY 527 GCAGCCCGCTCAAGCGGGAGTGGAGACCAACCAACCCCTCCAAACAAAGCAACAAGT 586
Db 632 GCAGCCCGCTCAAGCGGGAGTGGAGACCAACCAACCCCTCCAAACAAAGCAACAAGT 691
QY 587 ACAGCGCCAGCAGTACCTGAGCCTGACGCTGAGCAGTGGAGTCCCAAGAGCTACA 646
Db 692 ACAGCGCCAGCAGTATCTGAGCCTGAGCAGTGGAGTCCCAAGAGCTACA 751
QY 647 GCTGCCAGGTCAAGGAGGAGGAGCGCTGAGAGGAGCAGTGGCCCTTACAGATGTT 706
Db 752 GCTGCCAGGTCAAGGAGGAGGAGCGCTGAGAGGAGCAGTGGCCCTTACAGATGTT 811
QY 707 CAT 709
Db 812 CAT 814

RESULT 14
US-10-158-646-73
; Sequence 73, Application US/10158646
; Publication No. US20030073105A1
; GENERAL INFORMATION:

QY 433 TCCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTGTCTCTATAAGTCACTTCTAC 492
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Db 450 TCCTCTGAGGAGCTTCAAGCCCAACAGGCCACACTGGTGTGTCTCTATAAGTCACTTCTAC 509
|||
QY 493 CCGGGAGCCGTGACAGTGGCCCTGGAGGCGAGATAGCAGCCCCGTCAAGGCGGAGTGGAG 552
|||
Db 510 CCGGGAGCCGTGACAGTGGCCCTGGAGGCGAGATAGCAGCCCCGTCAAGGCGGAGTGGAG 569
|||
QY 553 ACCACCACACCCCTCCAAACAAAGCAACAACAAGTACGCGGCCGAGCACTACCTGAGCCTG 612
|||
Db 570 ACCACCACACCCCTCCAAACAAAGCAACAACAAGTACGCGGCCGAGCACTACCTGAGCCTG 629
|||
QY 613 AGCCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTACGCGATGAAGGAGC 672
|||
Db 630 AGCCTGAGCAGTGGAGTCCACAGAGCTACAGTGCAGGTACGCGATGAAGGAGC 689
|||
QY 673 ACCGTGGAGAAGACAGTGGCCCTACAGAAATGTTCA 709
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Db 690 ACCGTGGAGAAGACAGTGGCCCTACAGAAATGTTCA 726
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Search completed: June 3, 2003, 23:03:41
Job time : 95.7363 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 3, 2003, 14:26:38 ; Search time 40.5526 Seconds
(without alignments)
5376.898 Million cell updates/sec

Title: US-09-576-424-9
Perfect score: 711
Sequence: 1 atgagggtcccgctcagct.....ccctacagaatgttcacga 711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
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2: /cgn2_6/prodata/1/ina/5B-COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A-COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B-COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS-COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	711	3	US-08-487-550-9
2	582.6	81.9	935	3	US-09-049-672A-20
3	540.2	76.0	705	3	US-08-487-550-1
4	530.2	74.6	895	3	US-09-049-672A-25
5	510.6	71.8	891	3	US-09-049-672A-23
6	502.6	70.7	902	2	US-08-378-939-11
7	484.2	68.1	885	4	US-09-152-060-47
8	482.6	67.9	879	4	US-09-152-060-29
9	468.4	65.9	702	3	US-08-523-894-5
10	416.4	58.6	919	3	US-09-049-672A-24
11	412	57.9	928	4	US-09-152-060-46
12	367.4	51.7	716	4	US-08-793-450-5
13	323.6	45.5	584	4	US-09-404-879A-268
14	306.2	43.1	771	4	US-08-991-789A-241
15	306.2	43.1	771	4	US-09-062-451-241
16	306.4	43.1	771	4	US-09-598-326-241
17	264.4	37.2	408	4	US-09-025-769B-169
18	255.4	35.9	393	1	US-08-305-683A-3
19	254.8	35.8	933	4	US-09-079-029-8
20	253.2	35.6	642	2	US-08-634-783A-4
21	253.2	35.6	642	3	US-09-070-817-4
22	246.8	34.7	346	2	US-08-761-277A-50
23	244.2	34.3	330	4	US-09-240-274-132
24	242.4	34.1	318	2	US-08-646-981-4
25	242.4	34.1	333	2	US-08-477-553A-43
26	242.2	34.1	774	2	US-08-665-202-4
27	242.2	34.1	908	4	US-09-273-839A-9

28	241.2	33.9	327	4	US-09-240-274-223	Sequence 223, App
29	237.6	33.4	333	1	US-08-264-093-5	Sequence 5, Appl
30	236.6	33.3	396	2	US-08-345-321-3	Sequence 3, Appl
31	234.8	33.0	327	4	US-09-240-274-128	Sequence 128, App
32	233.2	32.8	327	4	US-09-240-274-126	Sequence 126, App
33	231.6	32.6	327	4	US-09-240-274-129	Sequence 129, App
34	231.6	32.6	327	4	US-09-240-274-130	Sequence 130, App
35	226.6	31.9	330	1	US-08-199-911-1	Sequence 1, Appl
36	226.6	31.9	336	4	US-09-240-274-133	Sequence 133, App
37	226.4	31.8	318	1	US-08-436-463-9	Sequence 9, Appl
38	226.4	31.8	318	1	US-08-024-253-9	Sequence 9, Appl
39	223	31.4	330	4	US-09-240-274-134	Sequence 134, App
40	220.4	31.0	327	4	US-09-240-274-123	Sequence 123, App
41	220.4	31.0	327	4	US-09-240-274-123	Sequence 123, App
42	217.4	30.6	342	4	US-09-240-274-131	Sequence 131, App
43	216.2	30.4	327	4	US-09-240-274-124	Sequence 124, App
44	208.8	29.4	333	2	US-08-652-816A-27	Sequence 27, Appl
45	204.4	28.7	327	4	US-09-240-274-127	Sequence 127, App

ALIGNMENTS

RESULT 1
US-08-487-550-9
; Sequence 9, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRINATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; FEATURE:
; MOLECULE TYPE: peptide
; NAME/KEY: CDS
; LOCATION: 1..711
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..711
US-08-487-550-9

Query Match 100.0%; Score 711; DB 3; Length 711;

APPLICATION NUMBER: 74.6%; Score 530.2; DB 3; Length 895;
FILING DATE: 87.5%; Pred. No. 2.3e-137;
ATTORNEY/AGENT INFORMATION: 0; Mismatches 83; Indels 0; Gaps 0;
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0355
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 895 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGTUT13
CLONE: 3116314
US-09-049-672A-25

Query Match 74.6%; Score 530.2; DB 3; Length 895;
Best Local Similarity 87.5%; Pred. No. 2.3e-137;
Matches 580; Conservative 0; Mismatches 83; Indels 0; Gaps 0;
QY 47 CAGGTGCACGATGTGAGTCTCTCTGACACAGCGCCCTCAGTGTCTGGGGCCCGCAGGCG 106
DB 80 CAGGTCCTGGCCCGAGTCTGTGCTGACTCAGCCCCCTCAGGCTTGGGACCCCGGCG 139
QY 107 AGAAGTCAACATCTGTGTCATCTGGAGCAGCTTCAACATTTGGAGTTATGATCTACATT 166
DB 140 AGAGGTCACCATCTCTTCTTCTGGAACCACTTCAACATCTGCAAGTAACTCTGTGCATT 199
QY 167 GTTACACAGCAGTCCCGAGGAGCGCCCAAACTCTCATCTATGACATTAACAGCGAC 226
DB 200 GTTACCAATTAGTTCAGAGGAGCGCCCAAACTCTCATCTATGATGATGACGCTG 259
QY 227 CTTCAAGGATTTCTGACCGATTTCTTGGTCTCAAGTCTGGTACCGCGGCTCCCTGGGCA 286
DB 260 CTTCCGGGTCTCTGACCGATTTCTTGGTCTCAAGTCTGGCAGCTCAGCTCCCTGGCA 319
QY 287 TCAGTGGGCTCAGACTGAGGATGAGGCTGATTTACTTGTGCAACATGGGATGACAGTG 346
DB 320 TCAGTGGGCTCAGGATGAGGATGAGGATGATTTACTTGTGCAACATGGGATGACAGTG 379
QY 347 TGAATGCTCAGATTTCTGAGGAGGAGGAGCGGCTGACGCTCTAGTCTGAGCCCAAGGCTG 406
DB 380 TCAGTGGTGGATGTTCCGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 439
QY 407 CCCCCCTCGTCACTCTGTTTCCCGCCCTCTCTGAGGAGCTTCAAGCCCAAGGCGCACAC 466
DB 440 CCCCCCTCGTCACTCTGTTTCCCACTCTCTGAGGAGCTTCAAGCCCAAGGCGCACAC 499
QY 467 TGGTGTCTCTAATAGTACTTCTTACCGGGAGCGCTGACAGTGGCTGGAAGGAGGATA 526
DB 500 TGGTGTCTCTAATAGTACTTCTTACCGGGAGCGCTGACAGTGGCTGGAAGGAGGATA 559
QY 527 CGAGCCCGCTCAAGGGGAGTGGAGACCAACACACCTTCCAAACAAAGCAACAAAGT 586
DB 560 CGAGCCCGCTCAAGGGGAGTGGAGACCAACACACCTTCCAAACAAAGCAACAAAGT 619
QY 587 AGCGGCCAGCAGTCACTGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 646
DB 620 AGCGGCCAGCAGTCACTGAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAGCTTCA 679
QY 647 GCTGCGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 706
DB 680 GCTGCGAGTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 739
QY 707 CAT 709
DB 740 CAT 742

RESULT 5

US-09-049-672A-23
Sequence 23, Application US/09049672A
Patent No. 6135941

GENERAL INFORMATION:

APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/049,672A

FILING DATE: HERewith

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Cerrone, Michael C

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0497 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 891 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: THYNOT10

CLONE: 2872705

US-09-049-672A-23

Query Match 71.8%; Score 510.6; DB 3; Length 891;

Best Local Similarity 84.5%; Pred. No. 6e-132;

Matches 599; Conservative 0; Mismatches 104; Indels 6; Gaps 2;

QY 4 AGGTCCTCGCTCAGCTCCTGGGCTCTGCTGCTCTGCTGCTCCAGGTGACGATGTGAG 63
DB 34 ATGGCTGGGCTGTGCTATTCTCACCCTCTCTCAGGGGCACAGGGTCTCTGGGCCCCAG 93
QY 64 TCTGTCTGACACAGCGCCCTCAGTGTCTGGGGCCCCAGGGGCACAGGTCAACATCTCG 123
DB 94 TCTGCTGTGATCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 153
QY 124 TGCCTGTGGAGCAGCTCCCAACATTTGGAGTTAT---GATCTACATTTGGTACGAGCTC 180
DB 154 TGCCTGTGGAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 213
QY 181 CCAGGACGGCCCCCAAACTCTCTATGACATTAACAGGACCTCAGGAATTTCT 240
DB 214 CCAGGACGGCCCCCAAACTCTATGATTTATGAGGTGAGTAAATCGGCTCAGGGGTTTCT 273


```

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-152-060-47

Query Match      58.1%; Score 484.2; DB 4; Length 885;
Best Local Similarity 80.8%; Pred. No. 1.2e-124;
Matches 564; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 13 GCTCAGCTCTGGGGCTCTGCTGCTCTGGCTCCAGGTGACGATGTGAGTCTGTCCTG 72
Db 30 GTTCTGCTCTCTGACCTCTCTCACTCACTGTGAGTGTGAGTGTCCAGGAGGGCTG 89
QY 73 ACACAGCGGCTCTGAGTGTCTGGGGCCCGAGGACGAGGTACCAATCTCTGTGCACTGGG 132
Db 90 ACTCAGCCCTCTGGGTGTCAAGGACTTGACAGACAGCCGCCACACTCACTGCAACGGG 149
QY 133 AGCACTTCAACATTGGAGGTATGATCTACATTTGATACAGCAGCTCCAGGACGGCC 192
Db 150 AACAAACAATGTTGGGACCAAGGAGGAGCTTGGCTGCAGCAGCAGGAGCCCT 209
QY 193 CCCAAACTCTCTATGACATTAACAAGCGACCTCAGGAATTTCTGACCGATTCTCT 252
Db 210 CCCAAACTCTGCTTACAGGATATATAACGGCCCTCAGGATCTCAGAGATTATCT 269
QY 253 GGTCTCAAGTGTGTTACCGCGCTCTCCCTGGCCATCATCTGGCTCCAGACTGAGGATGAG 312
Db 270 GCATCCAGGTCAGGAGCCACATCTCTCCCTGACCATTAATCTGGAATCCAGCTGAGGACGAG 329
QY 313 GCTGATTATTAATGTCAGTCTTATGACAGCAGCCTGAATGCTCAGTATTCGAGGAGGG 372
Db 330 GCTGATTATTAATGTCAGCAGCATATGACAGCAGCCTCGCAGTTGGAGTTGCGCGGAGGG 389
QY 373 ACCCGCTCAGCGTCTTAGTCTCAGCCCAAGGGTGGCCCTCGGTCACTCTGTTTCCCGCCC 432
Db 390 ACCAAGTCAAGCTCTTAGTCTCAGCCCAAGGGTGGCCCTCGGTCACTCTGTTTCCCGCCC 449
QY 433 TCCTCTGAGGAGTTCAAGCCCAACAGGCGCACACTGGTGTGTCTCATAGTCACTTCTAC 492
Db 450 TCCTCTGAGGAGTTCAAGCCCAACAGGCGCACACTGGTGTGTCTCATAGTCACTTCTAC 509
QY 493 CCGGAGCGCTGACAGTGTGCTGGAGGAGGAGTAGAGCCCGCTCAAGCGGGAGTGGAG 552
Db 510 CCGGAGCGCTGACAGTGTGCTGGAGGAGGAGTAGAGCCCGCTCAAGCGGGAGTGGAG 569

; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 28 Human Secreted Proteins
; FILE REFERENCE: P2003P1.US
; CURRENT APPLICATION NUMBER: US/09/152,060
; CURRENT FILING DATE: 1998-09-11
; EARLIER APPLICATION NUMBER: PCT/US98/04858
; EARLIER FILING DATE: 1998-03-12
; EARLIER APPLICATION NUMBER: 60/040,762
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/040,710
; EARLIER FILING DATE: 1997-03-14
; EARLIER APPLICATION NUMBER: 60/050,934
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,100
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,357
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/048,189
; EARLIER FILING DATE: 1997-05-30
; EARLIER APPLICATION NUMBER: 60/057,765
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/068,368
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 29
; LENGTH: 879
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-152-060-29

Query Match      67.9%; Score 482.6; DB 4; Length 879;
Best Local Similarity 80.8%; Pred. No. 3.2e-124;
Matches 563; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY 13 GCTCAGCTCTGGGGCTCTGCTGCTCTGGCTCCAGGTGACGATGTGAGTCTGTCCTG 72
Db 22 GTTCTGCTCTCTGACCTCTCTCACTCACTGTGAGTGTGAGTGTCCAGGAGGGCTG 81
QY 73 ACACAGCGGCTCTGAGTGTCTGGGGCCCGAGGACGAGGTACCAATCTCTGTGCACTGGG 132
Db 82 ACTCAGCCCTCTGGGTGTCCAAAGGACTTGAGACAGACCGCCACACTCACTGCAACGGG 141
QY 133 AGCACTTCAACATTGGAGGTATGATCTACATTTGATACAGCAGCTCCAGGACGGCC 192
Db 142 AACAAACAATGTTGGGACCAAGGAGGAGCTTGGCTGTCAGCAGCAGCAGGCGCACCT 201
QY 193 CCCAAACTCTCTATGACATTAACAAGCGACCTCAGGAATTTCTGACCGATTCTCT 252
Db 202 CCCAAACTCTCTGCTTACAGGATATATAACGGCCCTCAGGATCTCAGAGATTATCT 261
QY 253 GGTCTCAAGTGTGGTACCGCGCTCTCTGGCCATCACTGGGCTCCAGATGAGATGAG 312
```

[illegible]

RESULT 9

US-08-523-894-5
; Sequence 5, Application US/08523894
; Patent No. 6136310
; GENERAL INFORMATION:
; APPLICANT: Hanna, Nabil
; APPLICANT: Newman, Roland A.
; APPLICANT: Reff, Mitchell E.
; TITLE OF INVENTION: Recombinant Anti-CD4 Antibodies for Human
; TITLE OF INVENTION: Therapy
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314-3187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/523,894
; FILING DATE: 06-SEP-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 702 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/049,672A

FILING DATE: HEREMITH

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Carrone, Michael C.

REGISTRATION NUMBER: 39,132

REFERENCE/DOCKET NUMBER: PF-0497 US

TELEPHONE: 650-855-0555

TELEFAX: 650-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 919 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: LINDNOT08

CLONE: 3056213

US-09-049-672A-24

Query Match 58.6%; Score 416.4; DB 3; Length 919;

Best Local Similarity 78.7%; Pred. No. 6.3e-106;

Matches 524; Conservative 0; Mismatches 136; Indels 6; Gaps 2;

QY	47	CAGGTGCAGGATGTGAGTCTGCTGACACAGCGCCCTCAGTGTCTGGGGCCCGCAGGCG	106
DB	106	CAGGAGTGATCTCAGACTGTGGTGACCGAGGAGCCATGCTCAGTGTCCCTGGAG	165
QY	107	AGAAGTCAACATCTCGTGACCTGGGAGCAC---CTTCAACATTTGAGGTTATGATCTAC	163
DB	166	GGACAGTCAACATCTCGTGAGTCTGGCTCAGTCTCTACTAGTAACTACCCCA	225
QY	164	ATTGTTACAGAGTCTCCAGGACCGCCCCCAAACTCTCATCTATGACATTAACAGC	223
DB	226	GCTGTTACAGAGACCGCCCGCAGGCTCCACGACGCTCATATACGACAAAGTTTC	285
QY	224	GACCTCTCAGAAATTTCTGACCGATCTCTGGTCTCAAGTCTGACCGGCTCCCTGG	283
DB	286	GTCTCTGAGTCCCTGATGCTTCTCTGGTCCATCTTGGACAAAGCGGCTCA	345
QY	284	CCATCACTGGTCCAGACTGAGGATGAGGCTGATTTACTGCCAGTCTATGACAGCA	343
DB	346	CCATCACTGGGCGCCAGGAGATGATCTGATTTATTGTCCTATAT---AGGC	402
QY	344	GCCTGATGCTCAGGTATTTCGGAGGAGGACCGGCTGACCGTCTAGTCAAGCCAGG	403
DB	403	GTAGTGGCTCTTGGGTGTTTCGGCGGAGGAGCAAGCTGTCCTAGGTACGCCAAGG	462

QY	404	CTGCCCCCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCCAAAGGCCA	463
DB	463	CTGCCCCCTCGGTCACTCTGTTCCCACTCTCTCTGAGGAGCTTCAAGCCAAAGGCCA	522
QY	464	CACCTGGTGTCTCATAAGTGAATCTTACCCGGGAGCCGTGACAGTGGCTGGAAGGCAG	523
DB	523	CACCTGGTGTCTCATAAGTGAATCTTACCCGGGAGCCGTGACAGTGGCTGGAAGGCAG	582
QY	524	ATAGCAGCCCCCTCAAGGGGGAGTGGAGACCCACACACCTCCAAACAAAGCAACAACA	583
DB	583	ATAGCAGCCCCCTCAAGGGGGAGTGGAGACCCACACACCTCCAAACAAAGCAACAACA	642
QY	584	AGTACGCGGCCAGCAGCTACCTGAGCCTGAGCCCTGAGCAGTGGAGTCCCAACAGAGCT	643
DB	643	AGTACGCGGCCAGCAGCTACCTGAGCCTGAGCAGTGGAGTCCCAACAGAGCT	702
QY	644	ACAGCTGCCAGGTACCGCATGAAGGGAGGACCGTGGAGAAAGACAGTGGCCCTTACAGAT	703
DB	703	ACAGCTGCCAGGTACCGCATGAAGGGAGGACCGTGGAGAAAGACAGTGGCCCTTACAGAT	762
QY	704	GTTCAT 709	
DB	763	GTTCAT 768	

RESULT 11

US-09-152-060-46/c
Sequence 46, Application US/09152060
Patent No. 6448230
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003PI US
CURRENT APPLICATION NUMBER: US/09/152,060
CURRENT FILING DATE: 1998-09-11
EARLIER APPLICATION NUMBER: PCT/US98/04858
EARLIER FILING DATE: 1998-03-12
EARLIER APPLICATION NUMBER: 60/040,762
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/040,710
EARLIER FILING DATE: 1997-03-14
EARLIER APPLICATION NUMBER: 60/050,934
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,100
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,357
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/048,189
EARLIER FILING DATE: 1997-05-30
EARLIER APPLICATION NUMBER: 60/057,765
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/048,970
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/068,368
EARLIER FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 46
LENGTH: 928
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (49)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (78)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (148)

OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (163)
OTHER INFORMATION: n equals a,t,g, or c
FEATURE:
NAME/KEY: SITE
LOCATION: (532)
OTHER INFORMATION: n equals a,t,g, or c
US-09-152-060-46

Query Match 57.9%; Score 412; DB 4; Length 928;

Best Local Similarity 83.9%; Pred. No. 1e-104;

Matches 464; Conservative 18; Mismatches 69; Indels 2; Gaps 2;

QY 158 ATCTACATTTGGTACAGAGCTCCAGGACGGCCCC-CAAACTCTCTATCTATGACATT 216
DB 893 ATGTATTATTGGTACCAACAGAGTCAAGCCAGGCCCCCTGTGCTGTCTATGAGGAC 834
QY 217 ACAAGCGACCTCAGGATTTCTGACCGATTCTCTGGCTCCAGTCTGGTACCGGGCC 276
DB 833 AACAAACGACCTCCGG-ATCCCTSAGAGATTCTTGGCTCCAGTTCAGGGACAGTGGCC 775
QY 277 TCCTGGCCATCACTGGGCTCCAGACTGAGGATGAGGCTGATTATTACTGCCAGTCCAT 336
DB 774 ACTTGACTATCAGTGGGCCAGGTGGAGGATGGGCTGACTACTACTGTACTCAACA 715
QY 337 GACAGCAGCTGAATGCTCAGGTATTTCGGAGGAGGACCCGGCTGACCGTCTCTAGGTCA 396
DB 714 GACAGCAGTGGTAATCATGKGCTCTCGAATCGGACCAAGTCACTCTCTAGGTCA 655
QY 397 CCAAGGCTGCCCTCGGTCTACTCTGTTCCGCTCTCTCTGAGGAGTTCAGGCAAC 456
DB 654 CCAAGGCTGCCCTCGGTCTACTCTGTTCCGCTCTCTCTGAGGAGTTCAGGCAAC 595
QY 457 AAGGCACACTGGTGTCTCATAGTACTTCTACCGGGAGCGGTGACAGTGGCTGG 516
DB 594 AAGGCACACTGGTGTCTCATAGTACTTCTACCGGGAGCGGTGACAGTGGCTGG 535
QY 517 AAGGCAGATGACGCCCCCTCAAGGGGGAGTGGAGACCAACACACCTCCAAACAAAG 576
DB 534 AAGGCAGATGACGCCCCCTCAAGGGGGAGTGGAGACCAACACCTCCAAACAAAG 475
QY 577 AACAAAGTACGCGGCCAGCTACTGAGCTGACCGCTGACCGCTGAGAGTGGAGTCCAC 636
DB 474 AACAAAGTACGCGGCCAGCTACTGAGCTGACCGCTGAGCGTGGAGTGGAGTCCAC 415
QY 637 AAGGCTACAGTGCAGCTCAGCATGAGGAGGACCGGTGGAGAGAGTGGCGCT 696
DB 414 AAGGCTACAGTGCAGCTCAGCATGAGGAGGACCGGTGGAGAGAGTGGCGCT 355
QY 697 ACAGATGTTTCAT 709
DB 354 ACAGATGTTTCAT 342

RESULT 12

US-08-793-450-5

Sequence 5, Application US/08793450

Patent No. 6312690

GENERAL INFORMATION:

APPLICANT: EDELMAN, LENA

APPLICANT: MARGARITTE, CHRISTEL

APPLICANT: KACZOREK, MICHEL

APPLICANT: CHABATHI, HASSAN

TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D

TITLE OF INVENTION: 25

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

ADDRESSEE: P.C.

STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400

CITY: ARLINGTON

STATE: VA
COUNTRY: USA
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793.450
FILING DATE: 03-MAR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PR 94/10566
FILING DATE: 02-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: OBLON, NORMAN F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 660-118-0 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 716 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
FEATURE:
NAME/KEY: CDS
LOCATION: 1..716
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..57
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58..716
OTHER INFORMATION: /product= "IMMUNOGLOBIN, LIGHT"
OTHER INFORMATION: CHAIN"
US-08-793-450-5

Query Match 51.7%; Score 367.4; DB 4; Length 716;

Best Local Similarity 75.2%; Pred. No. 2e-92;

Matches 521; Conservative 0; Mismatches 121; Indels 51; Gaps 3;

QY 47 CAGGTGCAGATGTGCTGCTGCTGACACACGCGCCCTCAGTGTCTGGGGCCCCAGGGC 106
DB 44 CAGGTGTCTCCTCCGACATCGAGCTCACTCAGGACCTGTGTGTCTGTGGCTTGGGAC 103
QY 107 AGAAGGTCACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 166
DB 104 AGACAGTCAAGATCACATGCCAAGAGAGAGAGCTCA-----GAACTATTATGCAAGCT 157
QY 167 GGTACAGAGCTCCAGGAAAGCGGCCCCCAAACTCTCTATCTATGATGATGATGATGATGAT 226
DB 158 GGTACAG 217
QY 227 CCTCAGGATTTCTGACCGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 286
DB 218 CCTCAGGATTTCTGACCGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 277
QY 287 TCACCTGGGCTCCAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 346
DB 278 TCACCTGGGCTCCAGGAG 331
QY 347 TGAATGCTCAGGTATTTCGGAG 406
DB 332 -----AGGTGTTCCGAGGAG 382
QY 407 CCCCCCTCGTCACTCTGTGTTCCGCGCTCC-----T 436
DB 383 CCCCCCTCGTCACTCTGTGTTCCGCGCTCCCTCGAGGAGCTTCAAGCCAAAGAGCCACAC 442

QY 437 CTGAGGAGCTTCAAGCCAAACAGGCCACACTGGTGTCTCATAGTACTTCTACCCGG 496
DB 443 TCAGGAGCTTCAAGCCAAACAGGCCACACTAGTGTCTCATAGTACTTCTACCCGG 502
QY 497 GAGCCGTGACAGTGGCTTGAAGGAGATAGCAGCCCTCAAGGCGGAGTGGAGCCA 556
DB 503 GAGCTGTGACATTTGGCTTGAAGGAGATAGCAGCCCTCAAGGCGGAGTGGAGCCA 562
QY 557 CCACACCTTCCAAACAAAGCAACAAAGTACGCGGCCAGCAGCTACTCTGAGCCTGACGC 616
DB 563 ACAACCTTCCAAACAGAGCAACAAAGTACGCGGCCAGCAGCTACTCTGAGCCTGACGC 622
QY 617 CTGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGTCCAGCAGTACAGGAGGAGCAGC 676
DB 623 CCGAGCAGTGGAGTCCACAGAGCTACAGCTGCCAGTCCAGTCCAGTGAAGGAGCAGCTG 682
QY 677 TGGAGAGCAGTGGCCCTCAGAGATGTTTAT 709
DB 683 CAGAGAAGAGCGTGGCCCTCGAGAAATGTTTAT 715

RESULT 13
US-09-404-879A-268/c
; Sequence 268, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 268
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(584)
; OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-268

Query Match 45.5%; Score 323.6; DB 4; Length 584;
Best Local Similarity 87.3%; Pred. No. 2.3e-80;
Matches 378; Conservative 0; Mismatches 47; Indels 8; Gaps 2;

QY 220 AAGCGACCTCAGGAATTTCTGACCGATTCTCTGGCTCCAGTCTGGTAC-----CGCGG 274
DB 450 AAGCGCCCTCAGGGTCCCTGATCGTTTCTGGCTTCAAGTCTTGGCAACAGGGC 391
QY 275 CTCTCCTGCCATCACTGGGCTCCAGTCCAGTCCAGTCCAGTCCAGTCCAGTCC 334
DB 390 CTCTCCTTGACNGTCTCTGGGCTCCAGGCTGAGGATGAGGCTGATTACTCAGCTCAT 331
QY 335 ATGACAGAGCTGATGCTCAGGTATTCGGAGGAGGACCGGCTGACCTGCTAGGTTC 394
DB 330 ATGACAGGCAAC---AACAAATGGGTGTTCCGGGAGGAGCAAGCTGACCGCTTAGGTTC 274
QY 395 AGCCCAAGGCTGCCCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCA 454
DB 273 AGCCCAAGGCTGCCCTCGGTCACTCTGTTCCCGCCCTCTCTGAGGAGCTTCAAGCA 214
QY 455 ACAAGGCCACACTGGTGTCTCATAGTGAATTTTACCCGGAGCCGTGACAGTGGCT 514
DB 213 ACAAGGCCACACTGGTGTCTCATAGTGAATTTTACCCGGAGCCGTGACAGTGGCT 154
QY 515 GGAAGCAGATAGCAGCCCGTCAAGGCGGAGTGGAGACACACCTTCCAAACAA 574

DB 153 GGAAGCAGATAGCAGCCCGTCAAGGCGGAGTGGAGACACACACCTTCCAAACAA 94
QY 575 GCAACAAAGTACGCGGCCAGCAGCTACTGAGCTTACGCTGAGCAGTGGAAAGTCCC 634
DB 93 GCAACAAAGTACGCGGCCAGCAGCTACTGAGCTTACGCTGAGCAGTGGAAAGTCCC 34
QY 635 ACAGAGCTACAG 647
DB 33 ACAGAGCTACAG 21

RESULT 14
US-08-991-789A-241/c
; Sequence 241, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
; APPLICANT: Fridakis, Tony N.
; Smith, John M.
; Reed, Steven G.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF BREAST CANCER
; NUMBER OF SEQUENCES: 292
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,789A
; FILING DATE: 11-Dec-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
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; REGISTRATION NUMBER: 33,332
; REFERENCE/DOCKET NUMBER: 210121.419C3
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; INFORMATION FOR SEQ ID NO: 241:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; SEQUENCE DESCRIPTION: SEQ ID NO: 241:
US-08-991-789A-241

Query Match 43.1%; Score 306.2; DB 4; Length 771;
Best Local Similarity 83.7%; Pred. No. 1.6e-75;
Matches 370; Conservative 0; Mismatches 66; Indels 6; Gaps 2;

QY 122 CGTCACTGGGAGCAGCTCCAACTCTCATCTATGACATTAAACAGGACCTCAGGAATTT 178
DB 448 CTGCANTGGAACAGCAGTACGCTTGTGGTGTATAATAATGTCNTGGTACCAACAGC 389
QY 179 TCCAGGAGCGGCCCAACTCTCATCTATGACATTAAACAGGACCTCAGGAATTT 238
DB 388 ACCCAGGCAAGCCCAAAATTCATGATTTATGAGTTCGGTAATCGGCCCTCAGGGGTTT 329
QY 239 CTGACCCGATCTCTGGCTCCAAAGTCTGGTACCGGGCTCCCTGGCCATCACTTGGGCTCC 298
DB 328 CTATCGCTTCTTGGCTCCAAAGTNTGGCAACAGGCTCCCTGACCATCTCTGGGCTCC 269

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